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(54) Title: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION			
(57) Abstract <p>The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1_{LA1} gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.</p>			

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**METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION**

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4⁺ cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids
30 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion
35 capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4⁺ cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

5 Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell
10 death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly
15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of
20 each of these types. Infection of human CD-4⁺ T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.
25

30 HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and
35

replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I, -II, -III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4⁺ receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4⁺ cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the
5 successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991,
10 FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been
15 developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989,
20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs
25 which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4⁺ T-cells by some
30 HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,
35

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5 The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and
10 drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15 Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,
20 these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.
25 See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30 Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

35

3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and/or organisms other than HIV-1_{LAI}. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1_{LAI} transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and organisms other than HIV-1_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4⁺ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4⁺ cell-cell fusion (i.e.,
5 syncytial formation) and infection of CD-4⁺ cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral
25 sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the
30 invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

35

3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as
15 follows:

A (alanine)
R (arginine)
N (asparagine)
D (aspartic acid)
C (cysteine)
20 Q (glutamine)
E (glutamic acid)
G (glycine)
H (histidine)
I (isoleucine)
L (leucine)
K (lysine)
M (methionine)
25 F (phenylalanine)
P (proline)
S (serine)
T (threonine)
W (tryptophan)
Y (tyrosine)
V (valine)

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4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV_{LAI}; DP178 homologs derived from HIV-1_{SP2} (DP-185; SEQ ID:3), HIV-1_{RF} (SEQ ID:4), and HIV-1_{MDV} (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{rod} (SEQ ID:6) and HIV-2_{NDZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC₅₀ refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{8P2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5 FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

10 FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.

15 FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. 20 The proteins are more fully described, below, in Section 8.1.1.

 FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

25 FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PA178.

30 FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

35 FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5
5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

FIG. 20. Search results for HIV-1 (BRU
10 isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIP; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program
15 designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and
20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations
25 are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations
30 are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations
35 are as in FIG. 20.

FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor
10 HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D:
15 Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20 "-", negative antiviral activity;
 "+/-", antiviral activity at greater than 100µg/ml;
 "+", antiviral activity at between 50-100µg/ml;
 "++", antiviral activity at between 20-50µg/ml;
 "+++", antiviral activity at between 1-20µg/ml;
25 "++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

 "-", no helicity;
 "+", 25-50% helicity;
30 "++", 50-75% helicity;
 "++++", 75-100% helicity.

IC₅₀ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

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containing no peptide. IC_{50} values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. Purified peptides were used to obtain IC_{50} values, except where the values are marked by an asterisk (*), in which cases, the IC_{50} values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. Purified peptides were used to obtain IC_{50} values, except where the values are marked by an asterisk (*), in which cases, the IC_{50} values were obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined

by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

5 FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

10 FIG. 37. Motif search results for Pseudomonas aeruginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

15 FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

20 FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

25 FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

30 FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations are as in FIG. 20.

35

FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

5 FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides.

10 FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

15 FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC_{50} is as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

35

length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

intracellular processes involving coiled-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and
5 PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention
10 for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent
15 anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. In the HIV protein, gp41, DP178 corresponds to a putative α -helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal
20 site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It
25 is of interest that mutations in the C-terminal α -helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral
30 protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal α -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

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On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1_{LAI} isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH₂-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below.

Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ($-NH_2$) and "Z" may represent a carboxyl ($-COOH$) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE I
DP178 (SEQ ID:1) CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSL-Z
	X-YTSLI-Z
	X-YTSLIH-Z
5	X-YTSLIHS-Z
	X-YTSLIHSL-Z
	X-YTSLIHSLI-Z
	X-YTSLIHSLIE-Z
	X-YTSLIHSLIEE-Z
	X-YTSLIHSLIEES-Z
	X-YTSLIHSLIEESQ-Z
10	X-YTSLIHSLIEESQN-Z
	X-YTSLIHSLIEESQNNQ-Z
	X-YTSLIHSLIEESQNNQQ-Z
	X-YTSLIHSLIEESQNNQQE-Z
	X-YTSLIHSLIEESQNNQQEK-Z
	X-YTSLIHSLIEESQNNQQEKN-Z
	X-YTSLIHSLIEESQNNQQEKNE-Z
	X-YTSLIHSLIEESQNNQQEKNEQ-Z
15	X-YTSLIHSLIEESQNNQQEKNEQE-Z
	X-YTSLIHSLIEESQNNQQEKNEQEEL-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELL-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLE-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLEL-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELD-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDK-Z
20	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKW-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-S-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-SL-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-SLW-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-SLWN-Z
	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-SLWNW-Z
25	X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-SLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IA
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
5	X-SLWNWF-Z
	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
10	X-LELDKWASLWNWF-Z
	X-LLELDKWASLWNWF-Z
	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
15	X-QEKNEQELLELDKWASLWNWF-Z
	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQEKNEQELLELDKWASLWNWF-Z
	X-QNQEKNEQELLELDKWASLWNWF-Z
	X-SQNQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQEKNEQELLELDKWASLWNWF-Z
20	X-IEESQNQEKNEQELLELDKWASLWNWF-Z
	X-LIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to
5 peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral
10 activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability,
15 or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid
20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of
25 the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid
30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence
35 with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The
10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein
30 regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178
35 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the
5 resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations,
10 as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate
15 intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

20 5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to
25 residues 558 to 595 of HIV-1_{LA1} transmembrane (TM) gp41 protein, as shown here:

NH₂-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH
(SEQ ID:25)

30

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity
35 and/or the ability to modulate intracellular processes

involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ($-NH_2$) and "Z" may represent a carboxyl ($-COOH$) group. Alternatively, "X" may represent a hydrophobic group, including but not

10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or

15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred

20 "X" or "Z" macromolecular group is a peptide group.

25

30

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TABLE II
DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

	X-NNL-Z	
	X-NNLL-Z	
	X-NNLLR-Z	
5	X-NNLLRA-Z	
	X-NNLLRAI-Z	
	X-NNLLRAIE-Z	
	X-NNLLRAIEA-Z	
	X-NNLLRAIEAQ-Z	
	X-NNLLRAIEAQQ-Z	
	X-NNLLRAIEAQQH-Z	
10	X-NNLLRAIEAQQHL-Z	
	X-NNLLRAIEAQQHLL-Z	
	X-NNLLRAIEAQQHLLQ-Z	
	X-NNLLRAIEAQQHLLQL-Z	
	X-NNLLRAIEAQQHLLQLT-Z	
	X-NNLLRAIEAQQHLLQLTV-Z	
	X-NNLLRAIEAQQHLLQLTVW-Z	
	X-NNLLRAIEAQQHLLQLTVWQ-Z	
15	X-NNLLRAIEAQQHLLQLTVWQI-Z	
	X-NNLLRAIEAQQHLLQLTVWQIK-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQ-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQL-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z	
20	X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVR-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z	
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z	149
25	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z	148
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z	147
	X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z	

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.
- 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA
DP178 (SEQ ID:25) AMINO TRUNCATIONS
 → SIC: DP107

		X-KDQ- Z
		X-LKDQ- Z
5		X-YLKDQ- Z
		X-RYLKDQ- Z
		X-ERYLKDQ- Z
		X-VERYLKDQ- Z
		X-AVERYLKDQ- Z
		X-LAVERYLKDQ- Z
		X-ILAVERYLKDQ- Z
10		X-RILAVERYLKDQ- Z
		X-ARILAVERYLKDQ- Z
		X-QARILAVERYLKDQ- Z
		X-LQARILAVERYLKDQ- Z
		X-QLQARILAVERYLKDQ- Z
		X-KQLQARILAVERYLKDQ- Z
		X-IKQLQARILAVERYLKDQ- Z
		X-QIKQLQARILAVERYLKDQ- Z
15		X-WQIKQLQARILAVERYLKDQ- Z
		X-VWQIKQLQARILAVERYLKDQ- Z
		X-TVWQIKQLQARILAVERYLKDQ- Z
		X-LTVWQIKQLQARILAVERYLKDQ- Z
		X-QLTVWQIKQLQARILAVERYLKDQ- Z
		X-LQLTVWQIKQLQARILAVERYLKDQ- Z
		X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
20		X-HLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-QHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
	181	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
	180	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
25		X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
	179	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
		X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to
5 peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral
10 activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability,
15 or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid
20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of
25 the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid
30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence
35 with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The
10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein
30 regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107
35 region of the gp41 protein.

Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond
5 to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found,
10 or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (i.e., other
15 than HIV-1_{LA1}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41
20 peptide region of other (i.e., non HIV-1_{LA1}) HIV-1 isolates may include, for example, peptide sequences as shown below.

25 NH₂-YTNTIYTLLEESQNQQEKNEQEELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH₂-YTGIYNLLEESQNQQEKNEQEELLELDKWANLWNWF-COOH (SEQ ID:4);

30 NH₂-YTSLIYSLLEKSQIQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1_{SP1}, HIV-1_{RF}, and HIV-1_{MN} isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding
35 position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the
5 analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41
10 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178
15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2_{NH2} isolate has the 36 amino acid
20 sequence (reading from amino to carboxy terminus):

NH₂-LEANISQSLEQAQIQKEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations
25 of the HIV-2_{NH2} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right)
30 terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-
35 fluorenylmethoxy-carbonyl (Fmoc) group; or a

covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached
5 macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE IIIHIV-2_{NH2} DP178 analog carboxy truncations.

- X-LEA-Z
 X-LEAN-Z
 X-LEANI-Z
 X-LEANIS-Z
 5 X-LEANISQ-Z
 X-LEANISQS-Z
 X-LEANISQSL-Z
 X-LEANISQSLE-Z
 X-LEANISQSLEQ-Z
 X-LEANISQSLEQA-Z
 X-LEANISQSLEQAQ-Z
 10 X-LEANISQSLEQAQI-Z
 X-LEANISQSLEQAQIQ-Z
 X-LEANISQSLEQAQIQQ-Z
 X-LEANISQSLEQAQIQQE-Z
 X-LEANISQSLEQAQIQQEK-Z
 X-LEANISQSLEQAQIQQEK-N-Z
 X-LEANISQSLEQAQIQQEK-NM-Z
 X-LEANISQSLEQAQIQQEK-NMY-Z
 15 X-LEANISQSLEQAQIQQEK-NMYE-Z
 X-LEANISQSLEQAQIQQEK-NMYEL-Z
 X-LEANISQSLEQAQIQQEK-NMYELQ-Z
 X-LEANISQSLEQAQIQQEK-NMYELQK-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKL-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLN-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNS-Z
 20 X-LEANISQSLEQAQIQQEK-NMYELQKLNSW-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWD-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDV-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDVF-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDVFT-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDVFTN-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDVFTNW-Z
 X-LEANISQSLEQAQIQQEK-NMYELQKLNSWDVFTNWL-Z
 25

The one letter amino acid code is used.

Additionally,

- "X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxyl, dansyl, or
 30 T-butyloxycarbonyl; an acetyl group; a 9-
 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

- "Z" may represent a carboxyl group; an amido group; a
 T-butyloxycarbonyl group; a macromolecular carrier
 35 group including but not limited to lipid-fatty acid
 conjugates, polyethylene glycol, or carbohydrates.

TABLE IVHIV-2_{NDZ} DP178 analog amino truncations.

	X-NWL-Z
	X-TNWL-Z
	X-FTNWL-Z
5	X-VFTNWL-Z
	X-DVFTNWL-Z
	X-WDVFTNWL-Z
	X-SWDVFTNWL-Z
	X-NSWDVFTNWL-Z
	X-LNSWDVFTNWL-Z
	X-KLNSWDVFTNWL-Z
	X-QKLNSWDVFTNWL-Z
10	X-LQKLNSWDVFTNWL-Z
	X-ELQKLNSWDVFTNWL-Z
	X-YELQKLNSWDVFTNWL-Z
	X-MYELQKLNSWDVFTNWL-Z
	X-NMYELQKLNSWDVFTNWL-Z
	X-KNMYELQKLNSWDVFTNWL-Z
	X-EKNMYELQKLNSWDVFTNWL-Z
	X-QEKNMYELQKLNSWDVFTNWL-Z
15	X-QQEKNMYELQKLNSWDVFTNWL-Z
	X-IQQEKNMYELQKLNSWDVFTNWL-Z
	X-QIQQEKNMYELQKLNSWDVFTNWL-Z
	X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It
5 does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown
10 experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a
15 coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils
20 from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as
25 demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database
30 package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to
broad, as discussed in this Section and in Section 9,
35 with 107x178x4 being preferred. The sequences

identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are
 5 intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first
 10 position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by
 15 brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed
 20 or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

25 The ALLMOTI5 is written as follows:

```
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
```

30 Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth
 35 heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a
5 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in
10 Table VII, below at the end of this Section, being preferred.

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this
15 Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal
20 peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.
25 19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178
30 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino
35 acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

5 Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists
10 viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table
15 XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are
20 intended to be within the scope of the invention.

 The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify
25 substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in
30 Section 27 describes peptides with anti-simian immunodeficiency virus activity.

 The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178,
35 above, in Section 5.1. For example, these peptides

may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5 Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions
10 and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory
20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX
25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and
30 Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped
35 according to the specific virus which they inhibit,

including respiratory syncytial virus, human
parainfluenza virus 3, simian immunodeficiency virus
and measles virus.

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TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

PCGENE	ALLNOTES	AB Virus (as described)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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GENE	ALLNOTES	AB Name (see Serotype)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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PGENE	ALLNOTIS	ALL VIEWS (see Nucleotide)	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8
FILE NAME	PROTEIN	VIRUS	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8
PKP3A_PU3V	TYROSINE-PROTEIN KINASE TRANSFORMING PROT	PUMNARY SARCOMA VIRUS	61-99	132-231	141-218					
PKP3B_PU3V	TYROSINE-PROTEIN KINASE	ANISACIA MOOREI ENTOMOVIRUS	47-41							
PKP3C_PU3V	THYMIDINE KINASE	CAPRIPOXVIRUS (STRAIN KE-1)	38-43							
PKP3D_PU3V	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-1)	238-362	611-472						
PKP3E_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	90-124							
PKP3F_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN CL101)	90-124							
PKP3G_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN HFEA)	90-124							
PKP3H_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN KOS)	90-124							
PKP3I_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN SC16)	90-124							
PKP3J_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN 333)	91-125							
PKP3K_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 3/STRAIN WC11)	618-665							
PKP3L_PU3V	THYMIDINE KINASE	BOVINE HERPES VIRUS TYPE 3 (STRAIN WC11)	18-53	178-219						
PKP3M_PU3V	THYMIDINE KINASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN 1922)	16-53	178-219						
PKP3N_PU3V	THYMIDINE KINASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB17)	100-214							
PKP3O_PU3V	THYMIDINE KINASE	RELIN HERPESVIRUS (RELIN HERPESVIRUS 1)	53-86							
PKP3P_PU3V	THYMIDINE KINASE	MAJADOSSEY HERPESVIRUS	237-389							
PKP3Q_PU3V	THYMIDINE KINASE	HERPESVIRUS SAIMIRI (STRAIN 11)	69-103							
PKP3R_PU3V	THYMIDINE KINASE	PEUDODABIES VIRUS (STRAIN NIA-3)	161-202							
PKP3S_PU3V	THYMIDINE KINASE	AVIAN RETROVIRUS AD17	190-224							
PKP3T_PU3V	THYMIDINE KINASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	37-91	281-315						
PKP3U_PU3V	THYMIDINE KINASE	ICTALUNID HERPESVIRUS 1	487-528	597-621						
PKP3V_PU3V	THYMIDINE KINASE	MURINE SARCOMA VIRUS 3611	11-45							
PKP3W_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	127-168							
PKP3X_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	127-168							
PKP3Y_PU3V	THYMIDINE KINASE	VARIOLA VIRUS	127-171							
PKP3Z_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	147-181							
PKP3A_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	147-181							
PKP3B_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	189-203							
PKP3C_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	196-170							
PKP3D_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN L-147)	169-203							
PKP3E_PU3V	THYMIDINE KINASE	VARIOLA VIRUS	111-145							
PKP3F_PU3V	THYMIDINE KINASE	AVIAN SARCOMA VIRUS (STRAIN UN2)	13-46							
PKP3G_PU3V	THYMIDINE KINASE	AVIAN RETROVIRUS RPL30	13-46							
PKP3H_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	174-213							
PKP3I_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN Y17)	441-475							
PKP3J_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	223-264							
PKP3K_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	191-212	108-441						
PKP3L_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 40	199-213							
PKP3M_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 41	228-264	201-349						
PKP3N_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 2	228-264	201-349						
PKP3O_PU3V	THYMIDINE KINASE	HUMAN ADENOVIRUS TYPE 3	144-179	294-338						
PKP3P_PU3V	THYMIDINE KINASE	EPSTEIN-BARR VIRUS (STRAIN B95-1)	54-152	627-658						
PKP3Q_PU3V	THYMIDINE KINASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	1-41	627-657						
PKP3R_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-41	627-657						
PKP3S_PU3V	THYMIDINE KINASE	VARIOLA VIRUS	1-39	627-657						
PKP3T_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN COPENHAGEN)	72-137	245-284						
PKP3U_PU3V	THYMIDINE KINASE	VACCINIA VIRUS (STRAIN WR)	72-137	245-284						
PKP3V_PU3V	THYMIDINE KINASE	VARIOLA VIRUS	72-137	245-284						
PKP3W_PU3V	THYMIDINE KINASE	AFRICAN SWINE FEVER VIRUS (STRAIN BA11V)	116-137	278-313						
PKP3X_PU3V	THYMIDINE KINASE	ODONTOLISSUM RINGSPOT VIRUS	33-90							
PKP3Y_PU3V	THYMIDINE KINASE	PEPPER MILD MOTTLE VIRUS (STRAIN SPAIN)	76-66							
PKP3Z_PU3V	THYMIDINE KINASE	TOBACCO MILD GREEN MOSAIC VIRUS (STRAIN U.S.)	29-46							

[illegible]

[illegible]

CGENE	ALLNOTIS	AB Virus (not bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	VIRUS	50-91							
PR1A1	PR1A1	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A2	PR1A2	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A3	PR1A3	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A4	PR1A4	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A5	PR1A5	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A6	PR1A6	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A7	PR1A7	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A8	PR1A8	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A9	PR1A9	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A10	PR1A10	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A11	PR1A11	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A12	PR1A12	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A13	PR1A13	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A14	PR1A14	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A15	PR1A15	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A16	PR1A16	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A17	PR1A17	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A18	PR1A18	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A19	PR1A19	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A20	PR1A20	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A21	PR1A21	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A22	PR1A22	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A23	PR1A23	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A24	PR1A24	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A25	PR1A25	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A26	PR1A26	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A27	PR1A27	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A28	PR1A28	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A29	PR1A29	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A30	PR1A30	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A31	PR1A31	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A32	PR1A32	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A33	PR1A33	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A34	PR1A34	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A35	PR1A35	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A36	PR1A36	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A37	PR1A37	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A38	PR1A38	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A39	PR1A39	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A40	PR1A40	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A41	PR1A41	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A42	PR1A42	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A43	PR1A43	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A44	PR1A44	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A45	PR1A45	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A46	PR1A46	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A47	PR1A47	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A48	PR1A48	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A49	PR1A49	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A50	PR1A50	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A51	PR1A51	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A52	PR1A52	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A53	PR1A53	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A54	PR1A54	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A55	PR1A55	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A56	PR1A56	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A57	PR1A57	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A58	PR1A58	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A59	PR1A59	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A60	PR1A60	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A61	PR1A61	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A62	PR1A62	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A63	PR1A63	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A64	PR1A64	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A65	PR1A65	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A66	PR1A66	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A67	PR1A67	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A68	PR1A68	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A69	PR1A69	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A70	PR1A70	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A71	PR1A71	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A72	PR1A72	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A73	PR1A73	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A74	PR1A74	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A75	PR1A75	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A76	PR1A76	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A77	PR1A77	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A78	PR1A78	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A79	PR1A79	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A80	PR1A80	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A81	PR1A81	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A82	PR1A82	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A83	PR1A83	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A84	PR1A84	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A85	PR1A85	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A86	PR1A86	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A87	PR1A87	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A88	PR1A88	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A89	PR1A89	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A90	PR1A90	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A91	PR1A91	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A92	PR1A92	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A93	PR1A93	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A94	PR1A94	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A95	PR1A95	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A96	PR1A96	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A97	PR1A97	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A98	PR1A98	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A99	PR1A99	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A100	PR1A100	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A101	PR1A101	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A102	PR1A102	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A103	PR1A103	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A104	PR1A104	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A105	PR1A105	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A106	PR1A106	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A107	PR1A107	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A108	PR1A108	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A109	PR1A109	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A110	PR1A110	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A111	PR1A111	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A112	PR1A112	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A113	PR1A113	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A114	PR1A114	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A115	PR1A115	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A116	PR1A116	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A117	PR1A117	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A118	PR1A118	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A119	PR1A119	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A120	PR1A120	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A121	PR1A121	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A122	PR1A122	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A123	PR1A123	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A124	PR1A124	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A125	PR1A125	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A126	PR1A126	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A127	PR1A127	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A128	PR1A128	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A129	PR1A129	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A130	PR1A130	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A131	PR1A131	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A132	PR1A132	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A133	PR1A133	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A134	PR1A134	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A135	PR1A135	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A136	PR1A136	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A137	PR1A137	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A138	PR1A138	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A139	PR1A139	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A140	PR1A140	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A141	PR1A141	INFLUENZA A VIRUS (STRAIN A/ENGLAND/491)	50-91							
PR1A142	PR1A142	INFLUENZA A VIRUS (STRAIN A/								

[illegible]

[illegible]

[illegible]

[illegible]

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CC	CCNAME	ALLNOTES	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
1	PROTEIN	ALL VIREUS (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
2	PROTEIN	VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
3	PROTEIN	BOVINE RETROVIRUS SV-1	470-504	578-613						
4	PROTEIN	BOVINE RETROVIRUS (STRAIN 1314)	489-524	574-619						
5	PROTEIN	VIRUS LENTIVIRUS (STRAIN 1314) (CLONE LV1-1K31)	489-524	574-619						
6	PROTEIN	VIRUS LENTIVIRUS (STRAIN 1314) (CLONE LV1-1K32)	489-524	574-619						
7	PROTEIN	VIRUS LENTIVIRUS (STRAIN 1314) (CLONE LV1-1K33)	489-524	574-619						
8	PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-150	187-221						
9	PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN BR4)	132-200							
10	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN BR4)	20-79							
11	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN C1H)	81-95	142-201						
12	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	143-204	270-311						
13	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	143-204	270-311						
14	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	143-204	270-311						
15	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	143-204	270-311						
16	PROTEIN	MOUSE MAMMARY TUMOR VIRUS (STRAIN GR)	143-204	270-311						
17	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
18	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
19	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
20	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
21	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
22	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
23	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
24	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
25	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
26	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
27	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
28	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
29	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
30	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
31	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
32	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
33	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
34	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
35	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
36	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
37	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
38	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
39	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
40	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							
41	PROTEIN	BOVINE CYTOMEGALOVIRUS (STRAIN 1314)	13-31							

GENE	ALLNOTES	AI Virus (see biotriphage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	VIRUS								
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	HUMAN CYTOMEGALOVIRUS (STRAIN AD146)	037-441							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	16-110							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	HERPESVIRUS SABIRI (STRAIN 11)	324-343							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPEM14GEM)	347-403							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	347-403							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	367-403							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS (STRAIN DUDAS)	333-237							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	EPSTEIN-BARR VIRUS (STRAIN B95-4)	89-137							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	BOVINE HERPESVIRUS TYPE 1 (STRAIN 34)	101-135							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	106-140							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	HERPESVIRUS SAIMIRI (STRAIN 11)	123-139							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	SHOEPI FIBROSA VIRUS (STRAIN KASZA)	96-132							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPEM14GEM)	96-132							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN L-1V7)	96-132							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	96-132							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	171-212							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG53)	116-130							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPEM14GEM)	41-75							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	465-340							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	465-340							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPEM14GEM)	243-291							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	243-291							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	343-391							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	CAPRIPOXVIRUS (STRAIN KS-1)	19-40							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	COMPOX VIRUS	311-243							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPEM14GEM)	211-243							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	211-243							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPEM14GEM)	62-116							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	62-116							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	1-71							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPEM14GEM)	1-71							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	35-59							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	35-59							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPEM14GEM)	41-93							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPEM14GEM)	41-93							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	VARIOLA VIRUS	1533-1567							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	LELYSTAD VIRUS	1721-1758							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	EQUINE ARTERITIS VIRUS	1602-1117							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/ANN ARBOR/666)	1631-1473							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	330-391							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	279-313							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN A/BEIJING/1154)	171-242							
ADONUCLEOSIDE DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE DIPHOS									

[illegible]

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PCORE	ALLMOTIS	AD Virus (be bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	VIRUS	102-144							
PRPP_BABYA	RNA-DIRECTED RNA POLYMERASE	TORACCO NECROSIS VIRUS (STRAIN D)	102-144							
PRPP_CDVO	RNA POLYMERASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN AJ100)	99-158	160-216						
PRPP_HBLY	RNA POLYMERASE ALPHA SUBUNIT	CANDIDE DISTEMPOR VIRUS (STRAIN ONDERSTPOORT)	313-173							
PRPP_HBLY1	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS	99-158	160-216						
PRPP_HBLY2	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B) (STRAIN 1)	99-158	160-216						
PRPP_HBLY3	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	99-158	160-216						
PRPP_HBLY4	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A) (STRAIN 1)	99-158	160-216						
PRPP_HBLY5	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN EDENHONSTON)	315-374	460-495						
PRPP_HBLY6	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN IP-3-CA)	315-374	460-495						
PRPP_HBLY7	RNA POLYMERASE ALPHA SUBUNIT	MEASLES VIRUS (STRAIN YAKAGATA-1)	315-374	460-495						
PRPP_HBLY8	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN SBL-1)	109-183	213-275						
PRPP_HBLY9	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN ENDERS)	214-276							
PRPP_HBLY10	RNA POLYMERASE ALPHA SUBUNIT	MUMPS VIRUS (STRAIN MITSUAKA VACCINE)	214-276							
PRPP_HBLY11	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/21)	100-124							
PRPP_HBLY12	RNA POLYMERASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C45)	100-124							
PRPP_HBLY13	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C3)	60-114	313-364	375-437					
PRPP_HBLY14	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	60-114	313-364	375-437					
PRPP_HBLY15	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-573)	60-114	313-364	375-437					
PRPP_HBLY16	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-0930)	60-114	313-364	375-437					
PRPP_HBLY17	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS	218-281							
PRPP_HBLY18	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	218-281							
PRPP_HBLY19	RNA POLYMERASE ALPHA SUBUNIT	BOVINE PARAINFLUENZA 3 VIRUS	31-120	414-470						
PRPP_HBLY20	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 41815)	410-499							
PRPP_HBLY21	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	4-38	233-285						
PRPP_HBLY22	RNA POLYMERASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 64-333)	222-285							
PRPP_HBLY23	RNA POLYMERASE ALPHA SUBUNIT	PRY VIRUS	137-174							
PRPP_HBLY24	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN AVOI)	93-127							
PRPP_HBLY25	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN CYE-11)	93-127							
PRPP_HBLY26	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN EBA) AND (STRAIN PM)	93-127							
PRPP_HBLY27	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN PV)	93-127							
PRPP_HBLY28	RNA POLYMERASE ALPHA SUBUNIT	RABIES VIRUS (STRAIN SAD B19)	93-127							
PRPP_HBLY29	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 2 / HOST MUTANTS)	313-364	375-447						
PRPP_HBLY30	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 694)	313-364	375-447						
PRPP_HBLY31	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN FURUKAWA)	313-364	375-447						
PRPP_HBLY32	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN HARRIS)	313-364	375-447						
PRPP_HBLY33	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN 2)	313-364	375-447						
PRPP_HBLY34	RNA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS 3 (STRAIN W2)	305-278							
PRPP_HBLY35	RNA POLYMERASE ALPHA SUBUNIT	SONCHUS YELLOW NET VIRUS	138-173	233-281						
PRPP_HBLY36	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C1-43)	138-173							
PRPP_HBLY37	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN H1-43)	138-173							
PRPP_HBLY38	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	138-173							
PRPP_HBLY39	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	138-173							
PRPP_HBLY40	RNA POLYMERASE ALPHA SUBUNIT	VELOCULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	138-173							
PRPP_HBLY41	RNA POLYMERASE ALPHA SUBUNIT	VARICELLA ZOSTER VIRUS	223-284	361-395						
PRPP_HBLY42	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	21-46							
PRPP_HBLY43	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS	31-86							
PRPP_HBLY44	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	118-167	233-284						
PRPP_HBLY45	RNA POLYMERASE ALPHA SUBUNIT	VACCINIA VIRUS (STRAIN WR)	118-167	233-284						

Accession	Protein	Gene	Notes	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500
AB000001	ALLNOTES	ALLNOTES	ALLNOTES	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500
AB000002	ALLNOTES	ALLNOTES	ALLNOTES	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400</																																																																																																				

PCGENE	ALL MOTIFS	AD Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	HUMAN ADENOVIRUS TYPE 12	421-491	497-518						
ORNA TERMINAL PROTEIN	ORNA TERMINAL PROTEIN	AVIAN SARCOMA VIRUS (STRAIN 17)	310-314							
TRANSFORMING PROTEIN 10N	TRANSFORMING PROTEIN 10N	AVIAN MUSCULOPONEUROTIC FIBROSARCOMA VIRUS AS1Q	317-318	319-320						
TRANSFORMING PROTEIN 1AF	TRANSFORMING PROTEIN 1AF	SHOPE FIBROMA VIRUS (STRAIN KASZA)	327-333	329-310						
DNA TOPOISOMERASE II	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BA31V)	146-150	148-151	160-142	1133-1163				
DNA TOPOISOMERASE II	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 20V)	146-150	148-151	160-142	1133-1163				
POC-RELATED TRANSFORMING PROTEIN P18-515	POC-RELATED TRANSFORMING PROTEIN P18-515	SIMIAN SARCOMA VIRUS	16-71							
THYMIDYLATE SYNTHASE	THYMIDYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	315-260							
UBIQUITIN-LIKE PROTEIN	UBIQUITIN-LIKE PROTEIN	ORNGITA PSEUDOTUBUGATA MULTICAPSID POLYMEROSIS VIRUS	43-48							
HYPOHETICAL PROTEIN UL1	HYPOHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	180-203							
PROTEIN UL3	PROTEIN UL3	HERPES SIMPLEX VIRUS TYPE 1 (STRAIN 17)	84-128							
GENE 40 PROTEIN	GENE 40 PROTEIN	HERPES SIMPLEX VIRUS TYPE 2 (STRAIN HGS3)	82-126							
PROTEIN UL4	PROTEIN UL4	HERPES SIMPLEX VIRUS TYPE 1 (STRAIN AB-4P)	76-104							
PROTEIN UL5	PROTEIN UL5	HERPES SIMPLEX VIRUS TYPE 1 (STRAIN 17)	102-116							
PROTEIN UL6	PROTEIN UL6	HERPES SIMPLEX VIRUS (STRAIN B91-4)	104-143	313-347	376-410					
HYPOHETICAL PROTEIN UL6	HYPOHETICAL PROTEIN UL6	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-250							
PROTEIN UL7	PROTEIN UL7	HERPES SIMPLEX VIRUS TYPE 1 (STRAIN 17)	36-94	103-141	337-371	410-479				
PROTEIN UL8	PROTEIN UL8	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD-4P)	62-170	157-411	448-503					
PROTEIN UL9	PROTEIN UL9	HERPESVIRUS SAIMIRI (STRAIN 11)	90-140	151-194	303-316	364-403				
PROTEIN UL10	PROTEIN UL10	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	37-131	350-409	704-738					
HYPOHETICAL PROTEIN UL11	HYPOHETICAL PROTEIN UL11	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-10							
ORIGIN OF REPLICATION BINDING PROTEIN	ORIGIN OF REPLICATION BINDING PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD-4P)	174-208							
ORIGIN OF REPLICATION BINDING PROTEIN	ORIGIN OF REPLICATION BINDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163							
NONENSE	NONENSE									
HYPOHETICAL PROTEIN UL12	HYPOHETICAL PROTEIN UL12	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	37-81	183-227						
HYPOHETICAL PROTEIN UL14	HYPOHETICAL PROTEIN UL14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	305-343							
HYPOHETICAL GENE 43 PROTEIN	HYPOHETICAL GENE 43 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-4P)	32-96	246-283						
UL14 PROTEIN HOMOLOG	UL14 PROTEIN HOMOLOG	PSEUDORABIES VIRUS (STRAIN NIA-3)	61-91							
HYPOHETICAL GENE 44 PROTEIN	HYPOHETICAL GENE 44 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	61-103							
GENE 44 PROTEIN	GENE 44 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-4P)	366-300							
PROTEIN 108	PROTEIN 108	HERPES SIMPLEX VIRUS TYPE 6 / STRAIN UGANDA-1102	235-280							
GENE 40 PROTEIN	GENE 40 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-4P)	44-78	421-474						
HYPOHETICAL PROTEIN UL13	HYPOHETICAL PROTEIN UL13	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	213-253							
HYPOHETICAL PROTEIN UL14	HYPOHETICAL PROTEIN UL14	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-9							
PROTEIN UL14 HOMOLOG	PROTEIN UL14 HOMOLOG	INFECTION LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR)	161-193							
PROTEIN UL15	PROTEIN UL15	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	335-341	331-399						
PROTEIN UL16	PROTEIN UL16	HERPES SIMPLEX VIRUS TYPE 1 (STRAIN 17)	370-411							
PROTEIN UL17	PROTEIN UL17	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB-4P)	364-413							
PROTEIN UL18	PROTEIN UL18	HERPESVIRUS SAIMIRI (STRAIN 11)	39-93	183-221	365-406					
PROTEIN UL19	PROTEIN UL19	INFECTION LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIR)	183-221	183-221						
PROTEIN UL20	PROTEIN UL20	PSEUDORABIES VIRUS (STRAIN NIA-3)	246-283							

PGCENE	ALLIOTHS	All Viruses (see Bacteriophage Jpn)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS								
PUL37, HSV11	PROTEIN BOLF1	EPSTEIN-BARR VIRUS (STRAIN B95-1)	708-742							
PUL37, HSV8	PROTEIN UL37	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	831-891							
PUL37, HSV3A	GENE 31 PROTEIN	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD4P)	82-137			715-750	781-823			
PUL37, VZV0	GENE 63 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	6-43			687-741				
PUL37, HSV1A	GENE 31 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	719-753			786-837				
PUL41, VZV0	HYPOTHETICAL PROTEIN UL38	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-31							
PUL43, HSV11	HOT SHUTOFF PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	320-366							
PUL47, HSV8	DNA-BINDING PROTEIN UL41	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	134-168			231-263				
PUL47, HSV1A	DNA-BINDING GENE 13 PROTEIN	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD4P)	138-172							
PUL47, HSV4	HYPOTHETICAL PROTEIN UL43	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	72-109							
PUL47, VZV0	MEMBRANE PROTEIN UL40 HOMOLOG	EQUINE HERPES VIRUS TYPE 4 (STRAIN 1943)	37-48							
PUL43, HSV1K	GENE 13 MEMBRANE PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	312-383							
PUL45, HSV1M	PROTEIN UL43	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN K05)	96-137							
PUL47, HSV1A	PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AD4P)	86-137							
PUL47, HSV11	PROTEIN UL47	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	116-163			448-483				
PUL47, HSV1P	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	473-518							
PUL47, HSV8P	VIRION PROTEIN UL47	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F)	473-518							
PUL47, HSV6A	86.7 KD ALPHA TRANS-INDUCING PROTEIN	GOVINE HERPES VIRUS TYPE 1 (STRAIN PL-2)	361-412							
PUL47, HSV6B	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPES VIRUS TYPE 4 (STRAIN 1943)	193-246			382-620				
PUL47, VZV0	97 KD ALPHA TRANS-INDUCING PROTEIN	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD4P)	319-253			371-412				
PUL50, HSV1A	ALPHA TRANS-INDUCING FACTOR 91.8 KD PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	84-133			156-208				
PUL51, HSV11	PROTEIN UL50	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	155-189							
PUL51, HSV4	PROTEIN UL51	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	118-169							
PUL51, HSV8	GENE 8 PROTEIN	EQUINE HERPES VIRUS TYPE 4 (STRAIN 1942)	321-363							
PUL51, HSV1P	GENE 9 PROTEIN	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD4P)	120-161							
PUL53, EVR	GENE 7 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163							
PUL53, HSV11	PROBABLE DNA REPLICATION PROTEIN BSLF1	EPSTEIN-BARR VIRUS (STRAIN B95-1)	188-235							
PUL53, HSV8	DNA REPLICATION PROTEIN UL53	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	189-223							
PUL53, HSV3A	DNA REPLICATION PROTEIN UL53	EQUINE HERPES VIRUS TYPE 1 (STRAIN AD4P)	141-182			928-970				
PUL53, VZV0	PROBABLE DNA REPLICATION GENE 54 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	443-483							
PUL53, HSV1A	PROBABLE DNA REPLICATION GENE 8 PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	301-342							
PUL53, HSV2N	PROTEIN UL53	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	12-48							
PUL53, HSV11	PROTEIN UL53	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN H033)	151-183							
PUL53, HSV1A	PROBABLE DNA REPLICATION PROTEIN UL54	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	32-73							
PUL53, HSV1A	PROBABLE DNA REPLICATION PROTEIN UL70	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	39-99							
PUL57, HSV1A	HYPOTHETICAL PROTEIN UL74	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	43-79							
PUL57, HSV1A	HYPOTHETICAL PROTEIN 1R	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	235-270							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	346-400			912-916				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	357-391							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	26-38							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	107-144			188-222				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	79-116							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	101-145			174-216				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	88-122							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	23-37			299-314				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	34-51			259-293				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	73-151			213-230				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	51-103							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES SIMPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	45-100							
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HERPES VIRUS SAIMIRI (STRAIN 11)	6-40			758-792				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	130-171			330-364				
PUL58, HSV1A	HYPOTHETICAL GENE 24 PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	15-56			419-492	541-573			
PUL58, HSV1A	VIRION PROTEIN UL104	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)								

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[illegible]

PGCME	ALLIOTIS	AB Viruses (or Bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
FILE NAME	PROTEIN	VACCINIA VIRUS (STRAIN WR)	37-43	285-301	391-441																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					

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bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
TITLE NAME	PROTEIN	VIRUS	17-41																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														</																																																																																																																																																																																																																																																																																																																																																																																																									

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PROTEIN	ALLANTOIDS	AB Virus (see Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500
SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN GP120 PRECURSOR	SECRETORY GLYCOPROTEIN 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PCGENE	ALLNOTES	AB Virens (on Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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GENE	PROTEIN	ALLIOTIS	AB Virus (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA7	AREA1
VP1	VP1	VP1	VACCINIA VIRUS (STRAIN CURENIA GENI)	1-54						
VP2	VP2	VP2	REOVIRUS (TYPE 1) (STRAIN LANG)	117-211						
VP3	VP3	VP3	REOVIRUS (TYPE 3) (STRAIN DEARING)	416-450						
VP4	VP4	VP4	REOVIRUS (TYPE 3) (STRAIN DEARING)	416-450						
VP5	VP5	VP5	REOVIRUS (TYPE 3) (STRAIN DUROHES)	416-450						
VP6	VP6	VP6	REOVIRUS (TYPE 3) (STRAIN LANG)	416-450						
VP7	VP7	VP7	REOVIRUS (TYPE 3) (STRAIN LANG)	416-450						
VP8	VP8	VP8	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A31904)	41-90						
VP9	VP9	VP9	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A3)	41-90						
VP10	VP10	VP10	TURKEY RHINOTRACHEITIS VIRUS	16-70						
VP11	VP11	VP11	CANINE DISTEMPER VIRUS (STRAIN ONDOKS (POORT))	192-224						
VP12	VP12	VP12	INFLUENZA C VIRUS (STRAIN C/29/56)	71-114						
VP13	VP13	VP13	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA VICTORIA)	210-216						
VP14	VP14	VP14	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE C/43)	224-238						
VP15	VP15	VP15	BOVINE PARAINFLUENZA 3 VIRUS	99-133						
VP16	VP16	VP16	HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 31815)	99-133						
VP17	VP17	VP17	RABIES VIRUS (STRAIN A/01)	69-101						
VP18	VP18	VP18	RABIES VIRUS (STRAIN C/VE-11)	69-101						
VP19	VP19	VP19	RABIES VIRUS (STRAIN ERA)	69-101						
VP20	VP20	VP20	RABIES VIRUS (STRAIN MISHING/ABAR/RC/11)	69-101						
VP21	VP21	VP21	RABIES VIRUS (STRAIN PV)	69-101						
VP22	VP22	VP22	RABIES VIRUS (STRAIN SAD B19)	69-101						
VP23	VP23	VP23	SONCHIVUS YELLOW NET VIRUS	246-270						
VP24	VP24	VP24	VEICULAR STONATITIS VIRUS (ISOLATE INDIA 7) (STRAIN C)	199-232						
VP25	VP25	VP25	BOVINE CORONAVIRUS (STRAIN A/01)	171-209						
VP26	VP26	VP26	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (S)	212-237						
VP27	VP27	VP27	PORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS (S)	212-237						
VP28	VP28	VP28	PORCINE RESPIRATORY CORONAVIRUS (STRAIN B/41)	212-237						
VP29	VP29	VP29	TURKEY ENTERIC CORONAVIRUS	214-23						
VP30	VP30	VP30	HELPE INFECTION PERITONITIS VIRUS (STRAIN 19-1146)	212-237						
VP31	VP31	VP31	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN A/01)	212-237						
VP32	VP32	VP32	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN BEAUDETTE)	212-237						
VP33	VP33	VP33	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN BEAUDETTE)	212-237						
VP34	VP34	VP34	AVIAN INFECTION BRONCHITIS VIRUS (STRAIN C/01)	212-237						
VP35	VP35	VP35	EPSTEIN-BARR VIRUS (STRAIN B/01)	212-237						
VP36	VP36	VP36	CAULIFLOWER MOSAIC VIRUS (STRAIN C/11)	212-237						
VP37	VP37	VP37	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP38	VP38	VP38	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP39	VP39	VP39	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP40	VP40	VP40	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP41	VP41	VP41	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP42	VP42	VP42	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP43	VP43	VP43	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP44	VP44	VP44	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP45	VP45	VP45	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP46	VP46	VP46	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP47	VP47	VP47	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP48	VP48	VP48	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP49	VP49	VP49	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP50	VP50	VP50	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP51	VP51	VP51	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP52	VP52	VP52	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP53	VP53	VP53	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP54	VP54	VP54	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP55	VP55	VP55	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP56	VP56	VP56	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP57	VP57	VP57	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP58	VP58	VP58	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP59	VP59	VP59	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP60	VP60	VP60	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP61	VP61	VP61	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP62	VP62	VP62	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP63	VP63	VP63	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP64	VP64	VP64	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP65	VP65	VP65	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP66	VP66	VP66	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP67	VP67	VP67	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP68	VP68	VP68	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP69	VP69	VP69	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP70	VP70	VP70	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP71	VP71	VP71	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP72	VP72	VP72	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP73	VP73	VP73	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP74	VP74	VP74	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP75	VP75	VP75	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP76	VP76	VP76	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP77	VP77	VP77	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP78	VP78	VP78	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP79	VP79	VP79	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP80	VP80	VP80	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP81	VP81	VP81	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP82	VP82	VP82	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP83	VP83	VP83	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP84	VP84	VP84	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP85	VP85	VP85	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP86	VP86	VP86	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP87	VP87	VP87	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP88	VP88	VP88	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP89	VP89	VP89	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP90	VP90	VP90	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP91	VP91	VP91	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP92	VP92	VP92	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP93	VP93	VP93	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP94	VP94	VP94	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP95	VP95	VP95	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP96	VP96	VP96	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP97	VP97	VP97	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP98	VP98	VP98	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP99	VP99	VP99	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP100	VP100	VP100	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP101	VP101	VP101	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP102	VP102	VP102	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP103	VP103	VP103	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP104	VP104	VP104	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP105	VP105	VP105	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP106	VP106	VP106	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP107	VP107	VP107	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP108	VP108	VP108	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP109	VP109	VP109	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP110	VP110	VP110	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP111	VP111	VP111	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP112	VP112	VP112	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP113	VP113	VP113	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP114	VP114	VP114	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP115	VP115	VP115	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP116	VP116	VP116	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP117	VP117	VP117	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP118	VP118	VP118	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP119	VP119	VP119	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP120	VP120	VP120	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP121	VP121	VP121	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP122	VP122	VP122	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP123	VP123	VP123	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP124	VP124	VP124	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP125	VP125	VP125	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP126	VP126	VP126	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP127	VP127	VP127	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP128	VP128	VP128	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP129	VP129	VP129	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP130	VP130	VP130	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP131	VP131	VP131	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP132	VP132	VP132	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP133	VP133	VP133	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP134	VP134	VP134	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP135	VP135	VP135	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP136	VP136	VP136	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP137	VP137	VP137	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP138	VP138	VP138	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP139	VP139	VP139	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP140	VP140	VP140	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP141	VP141	VP141	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP142	VP142	VP142	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP143	VP143	VP143	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						
VP144	VP144	VP144	CAULIFLOWER MOSAIC VIRUS (STRAIN D/01)	212-237						

[illegible]

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[illegible]

PI TYPE	ALL VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
PI TYPE	ALL VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

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GENE	ALL VITIS	AD Virus (see Description page)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
GLYCOPROTEIN	ALL VITIS	AD Virus (see Description page)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
VP1	VP1	VP1	131-201	131-201	131-201	131-201	131-201	131-201	131-201	131-201
VP2	VP2	VP2	78-115	78-115	78-115	78-115	78-115	78-115	78-115	78-115
VP3	VP3	VP3	1-33	1-33	1-33	1-33	1-33	1-33	1-33	1-33
VP4	VP4	VP4	4-39	4-39	4-39	4-39	4-39	4-39	4-39	4-39
VP5	VP5	VP5	6-72	6-72	6-72	6-72	6-72	6-72	6-72	6-72
VP6	VP6	VP6	7-40	7-40	7-40	7-40	7-40	7-40	7-40	7-40
VP7	VP7	VP7	8-40	8-40	8-40	8-40	8-40	8-40	8-40	8-40
VP8	VP8	VP8	9-52	9-52	9-52	9-52	9-52	9-52	9-52	9-52
VP9	VP9	VP9	10-59	10-59	10-59	10-59	10-59	10-59	10-59	10-59
VP10	VP10	VP10	11-63	11-63	11-63	11-63	11-63	11-63	11-63	11-63
VP11	VP11	VP11	12-63	12-63	12-63	12-63	12-63	12-63	12-63	12-63
VP12	VP12	VP12	13-63	13-63	13-63	13-63	13-63	13-63	13-63	13-63
VP13	VP13	VP13	14-63	14-63	14-63	14-63	14-63	14-63	14-63	14-63
VP14	VP14	VP14	15-63	15-63	15-63	15-63	15-63	15-63	15-63	15-63
VP15	VP15	VP15	16-63	16-63	16-63	16-63	16-63	16-63	16-63	16-63
VP16	VP16	VP16	17-63	17-63	17-63	17-63	17-63	17-63	17-63	17-63
VP17	VP17	VP17	18-63	18-63	18-63	18-63	18-63	18-63	18-63	18-63
VP18	VP18	VP18	19-63	19-63	19-63	19-63	19-63	19-63	19-63	19-63
VP19	VP19	VP19	20-63	20-63	20-63	20-63	20-63	20-63	20-63	20-63
VP20	VP20	VP20	21-63	21-63	21-63	21-63	21-63	21-63	21-63	21-63
VP21	VP21	VP21	22-63	22-63	22-63	22-63	22-63	22-63	22-63	22-63
VP22	VP22	VP22	23-63	23-63	23-63	23-63	23-63	23-63	23-63	23-63
VP23	VP23	VP23	24-63	24-63	24-63	24-63	24-63	24-63	24-63	24-63
VP24	VP24	VP24	25-63	25-63	25-63	25-63	25-63	25-63	25-63	25-63
VP25	VP25	VP25	26-63	26-63	26-63	26-63	26-63	26-63	26-63	26-63
VP26	VP26	VP26	27-63	27-63	27-63	27-63	27-63	27-63	27-63	27-63
VP27	VP27	VP27	28-63	28-63	28-63	28-63	28-63	28-63	28-63	28-63
VP28	VP28	VP28	29-63	29-63	29-63	29-63	29-63	29-63	29-63	29-63
VP29	VP29	VP29	30-63	30-63	30-63	30-63	30-63	30-63	30-63	30-63
VP30	VP30	VP30	31-63	31-63	31-63	31-63	31-63	31-63	31-63	31-63
VP31	VP31	VP31	32-63	32-63	32-63	32-63	32-63	32-63	32-63	32-63
VP32	VP32	VP32	33-63	33-63	33-63	33-63	33-63	33-63	33-63	33-63
VP33	VP33	VP33	34-63	34-63	34-63	34-63	34-63	34-63	34-63	34-63
VP34	VP34	VP34	35-63	35-63	35-63	35-63	35-63	35-63	35-63	35-63
VP35	VP35	VP35	36-63	36-63	36-63	36-63	36-63	36-63	36-63	36-63
VP36	VP36	VP36	37-63	37-63	37-63	37-63	37-63	37-63	37-63	37-63
VP37	VP37	VP37	38-63	38-63	38-63	38-63	38-63	38-63	38-63	38-63
VP38	VP38	VP38	39-63	39-63	39-63	39-63	39-63	39-63	39-63	39-63
VP39	VP39	VP39	40-63	40-63	40-63	40-63	40-63	40-63	40-63	40-63
VP40	VP40	VP40	41-63	41-63	41-63	41-63	41-63	41-63	41-63	41-63
VP41	VP41	VP41	42-63	42-63	42-63	42-63	42-63	42-63	42-63	42-63
VP42	VP42	VP42	43-63	43-63	43-63	43-63	43-63	43-63	43-63	43-63
VP43	VP43	VP43	44-63	44-63	44-63	44-63	44-63	44-63	44-63	44-63
VP44	VP44	VP44	45-63	45-63	45-63	45-63	45-63	45-63	45-63	45-63
VP45	VP45	VP45	46-63	46-63	46-63	46-63	46-63	46-63	46-63	46-63
VP46	VP46	VP46	47-63	47-63	47-63	47-63	47-63	47-63	47-63	47-63
VP47	VP47	VP47	48-63	48-63	48-63	48-63	48-63	48-63	48-63	48-63
VP48	VP48	VP48	49-63	49-63	49-63	49-63	49-63	49-63	49-63	49-63
VP49	VP49	VP49	50-63	50-63	50-63	50-63	50-63	50-63	50-63	50-63
VP50	VP50	VP50	51-63	51-63	51-63	51-63	51-63	51-63	51-63	51-63
VP51	VP51	VP51	52-63	52-63	52-63	52-63	52-63	52-63	52-63	52-63
VP52	VP52	VP52	53-63	53-63	53-63	53-63	53-63	53-63	53-63	53-63
VP53	VP53	VP53	54-63	54-63	54-63	54-63	54-63	54-63	54-63	54-63
VP54	VP54	VP54	55-63	55-63	55-63	55-63	55-63	55-63	55-63	55-63
VP55	VP55	VP55	56-63	56-63	56-63	56-63	56-63	56-63	56-63	56-63
VP56	VP56	VP56	57-63	57-63	57-63	57-63	57-63	57-63	57-63	57-63
VP57	VP57	VP57	58-63	58-63	58-63	58-63	58-63	58-63	58-63	58-63
VP58	VP58	VP58	59-63	59-63	59-63	59-63	59-63	59-63	59-63	59-63
VP59	VP59	VP59	60-63	60-63	60-63	60-63	60-63	60-63	60-63	60-63
VP60	VP60	VP60	61-63	61-63	61-63	61-63	61-63	61-63	61-63	61-63
VP61	VP61	VP61	62-63	62-63	62-63	62-63	62-63	62-63	62-63	62-63
VP62	VP62	VP62	63-63	63-63	63-63	63-63	63-63	63-63	63-63	63-63
VP63	VP63	VP63	64-63	64-63	64-63	64-63	64-63	64-63	64-63	64-63
VP64	VP64	VP64	65-63	65-63	65-63	65-63	65-63	65-63	65-63	65-63
VP65	VP65	VP65	66-63	66-63	66-63	66-63	66-63	66-63	66-63	66-63
VP66	VP66	VP66	67-63	67-63	67-63	67-63	67-63	67-63	67-63	67-63
VP67	VP67	VP67	68-63	68-63	68-63	68-63	68-63	68-63	68-63	68-63
VP68	VP68	VP68	69-63	69-63	69-63	69-63	69-63	69-63	69-63	69-63
VP69	VP69	VP69	70-63	70-63	70-63	70-63	70-63	70-63	70-63	70-63
VP70	VP70	VP70	71-63	71-63	71-63	71-63	71-63	71-63	71-63	71-63
VP71	VP71	VP71	72-63	72-63	72-63	72-63	72-63	72-63	72-63	72-63
VP72	VP72	VP72	73-63	73-63	73-63	73-63	73-63	73-63	73-63	73-63
VP73	VP73	VP73	74-63	74-63	74-63	74-63	74-63	74-63	74-63	74-63
VP74	VP74	VP74	75-63	75-63	75-63	75-63	75-63	75-63	75-63	75-63
VP75	VP75	VP75	76-63	76-63	76-63	76-63	76-63	76-63	76-63	76-63
VP76	VP76	VP76	77-63	77-63	77-63	77-63	77-63	77-63	77-63	77-63
VP77	VP77	VP77	78-63	78-63	78-63	78-63	78-63	78-63	78-63	78-63
VP78	VP78	VP78	79-63	79-63	79-63	79-63	79-63	79-63	79-63	79-63
VP79	VP79	VP79	80-63	80-63	80-63	80-63	80-63	80-63	80-63	80-63
VP80	VP80	VP80	81-63	81-63	81-63	81-63	81-63	81-63	81-63	81-63
VP81	VP81	VP81	82-63	82-63	82-63	82-63	82-63	82-63	82-63	82-63
VP82	VP82	VP82	83-63	83-63	83-63	83-63	83-63	83-63	83-63	83-63
VP83	VP83	VP83	84-63	84-63	84-63	84-63	84-63	84-63	84-63	84-63
VP84	VP84	VP84	85-63	85-63	85-63	85-63	85-63	85-63	85-63	85-63
VP85	VP85	VP85	86-63	86-63	86-63	86-63	86-63	86-63	86-63	86-63
VP86	VP86	VP86	87-63	87-63	87-63	87-63	87-63	87-63	87-63	87-63
VP87	VP87	VP87	88-63	88-63	88-63	88-63	88-63	88-63	88-63	88-63
VP88	VP88	VP88	89-63	89-63	89-63	89-63	89-63	89-63	89-63	89-63
VP89	VP89	VP89	90-63	90-63	90-63	90-63	90-63	90-63	90-63	90-63
VP90	VP90	VP90	91-63	91-63	91-63	91-63	91-63	91-63	91-63	91-63
VP91	VP91	VP91	92-63	92-63	92-63	92-63	92-63	92-63	92-63	92-63
VP92	VP92	VP92	93-63	93-63	93-63	93-63	93-63	93-63	93-63	93-63
VP93	VP93	VP93	94-63	94-63	94-63	94-63	94-63	94-63	94-63	94-63
VP94	VP94	VP94	95-63	95-63	95-63	95-63	95-63	95-63	95-63	95-63
VP95	VP95	VP95	96-63	96-63	96-63	96-63	96-63	96-63	96-63	96-63
VP96	VP96	VP96	97-63	97-63	97-63	97-63	97-63	97-63	97-63	97-63
VP97	VP97	VP97	98-63	98-63	98-63	98-63	98-63	98-63	98-63	98-63
VP98	VP98	VP98	99-63	99-63	99-63	99-63	99-63	99-63	99-63	99-63
VP99	VP99	VP99	100-63	100-63	100-63	100-63	100-63	100-63	100-63	100-63

[illegible]

GENE	ALLIOTIS	AB Virus (on bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	REOVIRUS (TYPE 1) (STRAIN LANG)	3-107							
SIGMA 1 PROTEIN	SIGMA 1 PROTEIN	REOVIRUS (TYPE 1) (STRAIN DEADING)	350-384							
SIGMA 2 PROTEIN	SIGMA 2 PROTEIN	REOVIRUS (TYPE 1) (STRAIN LANG)	350-384							
SIGMA 3 PROTEIN	SIGMA 3 PROTEIN	REOVIRUS (TYPE 1) (STRAIN DEADING)	35-119							
SIGMA 4 PROTEIN	SIGMA 4 PROTEIN	REOVIRUS (TYPE 1) (STRAIN DEADING)	7-43							
SIGMA 5 PROTEIN	SIGMA 5 PROTEIN	REOVIRUS (TYPE 1) (STRAIN DEADING)	318-333							
STRUCTURAL PROTEIN 1 PRECURSOR	STRUCTURAL PROTEIN 1 PRECURSOR	HEPATITIS E VIRUS (STRAIN BURMA) (HEV)	317-331							
STRUCTURAL PROTEIN 2 PRECURSOR	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIRUS (STRAIN KENYON) (HEV)	318-333							
STRUCTURAL PROTEIN 3 PRECURSOR	STRUCTURAL PROTEIN 3 PRECURSOR	HEPATITIS E VIRUS (STRAIN NYANGAR) (HEV)	318-333							
STRUCTURAL PROTEIN 4 PRECURSOR	STRUCTURAL PROTEIN 4 PRECURSOR	HEPATITIS E VIRUS (STRAIN PAKISTAN) (HEV)	180-220							
STRUCTURAL PROTEIN 5	STRUCTURAL PROTEIN 5	HEPATITIS E VIRUS (ISOLATE RHESUS) (HEV)	120-158							
PROTEIN 1A	PROTEIN 1A	CAPRIPOX VIRUS (STRAIN INS-1)	80-120							
PROTEIN 1B	PROTEIN 1B	CAPRIPOX VIRUS (STRAIN INS-1)	80-120							
PROTEIN 1C	PROTEIN 1C	CAPRIPOX VIRUS (STRAIN INS-1)	317-399							
PROTEIN 1D	PROTEIN 1D	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1E	PROTEIN 1E	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1F	PROTEIN 1F	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1G	PROTEIN 1G	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1H	PROTEIN 1H	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1I	PROTEIN 1I	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1J	PROTEIN 1J	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1K	PROTEIN 1K	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1L	PROTEIN 1L	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1M	PROTEIN 1M	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1N	PROTEIN 1N	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1O	PROTEIN 1O	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1P	PROTEIN 1P	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1Q	PROTEIN 1Q	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1R	PROTEIN 1R	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1S	PROTEIN 1S	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1T	PROTEIN 1T	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1U	PROTEIN 1U	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1V	PROTEIN 1V	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1W	PROTEIN 1W	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1X	PROTEIN 1X	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1Y	PROTEIN 1Y	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 1Z	PROTEIN 1Z	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2A	PROTEIN 2A	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2B	PROTEIN 2B	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2C	PROTEIN 2C	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2D	PROTEIN 2D	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2E	PROTEIN 2E	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2F	PROTEIN 2F	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2G	PROTEIN 2G	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2H	PROTEIN 2H	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2I	PROTEIN 2I	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2J	PROTEIN 2J	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2K	PROTEIN 2K	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2L	PROTEIN 2L	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2M	PROTEIN 2M	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2N	PROTEIN 2N	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2O	PROTEIN 2O	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2P	PROTEIN 2P	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2Q	PROTEIN 2Q	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2R	PROTEIN 2R	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2S	PROTEIN 2S	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2T	PROTEIN 2T	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2U	PROTEIN 2U	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2V	PROTEIN 2V	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2W	PROTEIN 2W	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2X	PROTEIN 2X	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2Y	PROTEIN 2Y	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 2Z	PROTEIN 2Z	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3A	PROTEIN 3A	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3B	PROTEIN 3B	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3C	PROTEIN 3C	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3D	PROTEIN 3D	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3E	PROTEIN 3E	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3F	PROTEIN 3F	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3G	PROTEIN 3G	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3H	PROTEIN 3H	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3I	PROTEIN 3I	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3J	PROTEIN 3J	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3K	PROTEIN 3K	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3L	PROTEIN 3L	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3M	PROTEIN 3M	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3N	PROTEIN 3N	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3O	PROTEIN 3O	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3P	PROTEIN 3P	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3Q	PROTEIN 3Q	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3R	PROTEIN 3R	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3S	PROTEIN 3S	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3T	PROTEIN 3T	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3U	PROTEIN 3U	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3V	PROTEIN 3V	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3W	PROTEIN 3W	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3X	PROTEIN 3X	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3Y	PROTEIN 3Y	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 3Z	PROTEIN 3Z	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4A	PROTEIN 4A	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4B	PROTEIN 4B	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4C	PROTEIN 4C	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4D	PROTEIN 4D	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4E	PROTEIN 4E	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4F	PROTEIN 4F	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4G	PROTEIN 4G	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4H	PROTEIN 4H	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4I	PROTEIN 4I	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4J	PROTEIN 4J	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4K	PROTEIN 4K	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4L	PROTEIN 4L	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4M	PROTEIN 4M	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4N	PROTEIN 4N	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4O	PROTEIN 4O	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4P	PROTEIN 4P	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4Q	PROTEIN 4Q	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4R	PROTEIN 4R	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4S	PROTEIN 4S	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4T	PROTEIN 4T	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4U	PROTEIN 4U	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4V	PROTEIN 4V	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4W	PROTEIN 4W	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4X	PROTEIN 4X	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4Y	PROTEIN 4Y	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 4Z	PROTEIN 4Z	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5A	PROTEIN 5A	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5B	PROTEIN 5B	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5C	PROTEIN 5C	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5D	PROTEIN 5D	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5E	PROTEIN 5E	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5F	PROTEIN 5F	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5G	PROTEIN 5G	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5H	PROTEIN 5H	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5I	PROTEIN 5I	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-631							
PROTEIN 5J	PROTEIN 5J	EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN) (HERPESVIRUS 4)	617-6							

REGION	GENE	PROTEIN	AB Type (no description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCGENE	ALLNOTIS	All Viruses (no Battelaphages)	AREA1	AREA1	AREA1	AREA1	AREA1	AREA1	AREA1
ELC XAIE	PROTEIN	VIRUS	31-51						
PY1BH VACCC	HYPOTHETICAL 19 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-39						
PY1YC VACCC	HYPOTHETICAL 14 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	11-48						
PY1DB VACCC	HYPOTHETICAL 93 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	39-80						
PY1DB VACCV	HYPOTHETICAL 93 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	46-80						
PY1DC VACCV	HYPOTHETICAL 93 KD PROTEIN	VACCINIA VIRUS (STRAIN WR)	7-41						
PY1DB VACCC	HYPOTHETICAL 11 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	10-51						
PY1TA VACCC	HYPOTHETICAL 11 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	9-53						

TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

[illegible]

GENE	1974-1984	AD Virus (as batiflagh-201)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 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673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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[illegible]

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Accession	Gene	Protein	1971-1974	1975-1979	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014	2015-2019	2020-2024	2025-2029	2030-2034	2035-2039	2040-2044	2045-2049	2050-2054	2055-2059	2060-2064	2065-2069	2070-2074	2075-2079	2080-2084	2085-2089	2090-2094	2095-2099	2100-2104	2105-2109	2110-2114	2115-2119	2120-2124	2125-2129	2130-2134	2135-2139	2140-2144	2145-2149	2150-2154	2155-2159	2160-2164	2165-2169	2170-2174	2175-2179	2180-2184	2185-2189	2190-2194	2195-2199	2200-2204	2205-2209	2210-2214	2215-2219	2220-2224	2225-2229	2230-2234	2235-2239	2240-2244	2245-2249	2250-2254	2255-2259	2260-2264	2265-2269	2270-2274	2275-2279	2280-2284	2285-2289	2290-2294	2295-2299	2300-2304	2305-2309	2310-2314	2315-2319	2320-2324	2325-2329	2330-2334	2335-2339	2340-2344	2345-2349	2350-2354	2355-2359	2360-2364	2365-2369	2370-2374	2375-2379	2380-2384	2385-2389	2390-2394	2395-2399	2400-2404	2405-2409	2410-2414	2415-2419	2420-2424	2425-2429	2430-2434	2435-2439	2440-2444	2445-2449	2450-2454	2455-2459	2460-2464	2465-2469	2470-2474	2475-2479	2480-2484	2485-2489	2490-2494	2495-2499	2500-2504	2505-2509	2510-2514	2515-2519	2520-2524	2525-2529	2530-2534	2535-2539	2540-2544	2545-2549	2550-2554	2555-2559	2560-2564	2565-2569	2570-2574	2575-2579	2580-2584	2585-2589	2590-2594	2595-2599	2600-2604	2605-2609	2610-2614	2615-2619	2620-2624	2625-2629	2630-2634	2635-2639	2640-2644	2645-2649	2650-2654	2655-2659	2660-2664	2665-2669	2670-2674	2675-2679	2680-2684	2685-2689	2690-2694	2695-2699	2700-2704	2705-2709	2710-2714	2715-2719	2720-2724	2725-2729	2730-2734	2735-2739	2740-2744	2745-2749	2750-2754	2755-2759	2760-2764	2765-2769	2770-2774	2775-2779	2780-2784	2785-2789	2790-2794	2795-2799	2800-2804	2805-2809	2810-2814	2815-2819	2820-2824	2825-2829	2830-2834	2835-2839	2840-2844	2845-2849	2850-2854	2855-2859	2860-2864	2865-2869	2870-2874	2875-2879	2880-2884	2885-2889	2890-2894	2895-2899	2900-2904	2905-2909	2910-2914	2915-2919	2920-2924	2925-2929	2930-2934	2935-2939	2940-2944	2945-2949	2950-2954	2955-2959	2960-2964	2965-2969	2970-2974	2975-2979	2980-2984	2985-2989	2990-2994	2995-2999	3000-3004	3005-3009	3010-3014	3015-3019	3020-3024	3025-3029	3030-3034	3035-3039	3040-3044	3045-3049	3050-3054	3055-3059	3060-3064	3065-3069	3070-3074	3075-3079	3080-3084	3085-3089	3090-3094	3095-3099	3100-3104	3105-3109	3110-3114	3115-3119	3120-3124	3125-3129	3130-3134	3135-3139	3140-3144	3145-3149	3150-3154	3155-3159	3160-3164	3165-3169	3170-3174	3175-3179	3180-3184	3185-3189	3190-3194	3195-3199	3200-3204	3205-3209	3210-3214	3215-3219	3220-3224	3225-3229	3230-3234	3235-3239	3240-3244	3245-3249	3250-3254	3255-3259	3260-3264	3265-3269	3270-3274	3275-3279	3280-3284	3285-3289	3290-3294	3295-3299	3300-3304	3305-3309	3310-3314	3315-3319	3320-3324	3325-3329	3330-3334	3335-3339	3340-3344	3345-3349	3350-3354	3355-3359	3360-3364	3365-3369	3370-3374	3375-3379	3380-3384	3385-3389	3390-3394	3395-3399	3400-3404	3405-3409	3410-3414	3415-3419	34
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GENE	1978/1984	ALL Viruses (see Introduction)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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37	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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GENE	1951/52	1953/54	1955/56	1957/58	1959/60	1961/62	1963/64	1965/66	1967/68	1969/70	1971/72	1973/74	1975/76	1977/78	1979/80	1981/82	1983/84	1985/86	1987/88	1989/90	1991/92	1993/94	1995/96	1997/98	1999/00	2001/02	2003/04	2005/06	2007/08	2009/10	2011/12	2013/14	2015/16	2017/18	2019/20	2021/22	2023/24	2025/26	2027/28	2029/30	2031/32	2033/34	2035/36	2037/38	2039/40	2041/42	2043/44	2045/46	2047/48	2049/50	2051/52	2053/54	2055/56	2057/58	2059/60	2061/62	2063/64	2065/66	2067/68	2069/70	2071/72	2073/74	2075/76	2077/78	2079/80	2081/82	2083/84	2085/86	2087/88	2089/90	2091/92	2093/94	2095/96	2097/98	2099/00	2101/02	2103/04	2105/06	2107/08	2109/10	2111/12	2113/14	2115/16	2117/18	2119/20	2121/22	2123/24	2125/26	2127/28	2129/30	2131/32	2133/34	2135/36	2137/38	2139/40	2141/42	2143/44	2145/46	2147/48	2149/50	2151/52	2153/54	2155/56	2157/58	2159/60	2161/62	2163/64	2165/66	2167/68	2169/70	2171/72	2173/74	2175/76	2177/78	2179/80	2181/82	2183/84	2185/86	2187/88	2189/90	2191/92	2193/94	2195/96	2197/98	2199/00	2201/02	2203/04	2205/06	2207/08	2209/10	2211/12	2213/14	2215/16	2217/18	2219/20	2221/22	2223/24	2225/26	2227/28	2229/30	2231/32	2233/34	2235/36	2237/38	2239/40	2241/42	2243/44	2245/46	2247/48	2249/50	2251/52	2253/54	2255/56	2257/58	2259/60	2261/62	2263/64	2265/66	2267/68	2269/70	2271/72	2273/74	2275/76	2277/78	2279/80	2281/82	2283/84	2285/86	2287/88	2289/90	2291/92	2293/94	2295/96	2297/98	2299/00	2301/02	2303/04	2305/06	2307/08	2309/10	2311/12	2313/14	2315/16	2317/18	2319/20	2321/22	2323/24	2325/26	2327/28	2329/30	2331/32	2333/34	2335/36	2337/38	2339/40	2341/42	2343/44	2345/46	2347/48	2349/50	2351/52	2353/54	2355/56	2357/58	2359/60	2361/62	2363/64	2365/66	2367/68	2369/70	2371/72	2373/74	2375/76	2377/78	2379/80	2381/82	2383/84	2385/86	2387/88	2389/90	2391/92	2393/94	2395/96	2397/98	2399/00	2401/02	2403/04	2405/06	2407/08	2409/10	2411/12	2413/14	2415/16	2417/18	2419/20	2421/22	2423/24	2425/26	2427/28	2429/30	2431/32	2433/34	2435/36	2437/38	2439/40	2441/42	2443/44	2445/46	2447/48	2449/50	2451/52	2453/54	2455/56	2457/58	2459/60	2461/62	2463/64	2465/66	2467/68	2469/70	2471/72	2473/74	2475/76	2477/78	2479/80	2481/82	2483/84	2485/86	2487/88	2489/90	2491/92	2493/94	2495/96	2497/98	2499/00	2501/02	2503/04	2505/06	2507/08	2509/10	2511/12	2513/14	2515/16	2517/18	2519/20	2521/22	2523/24	2525/26	2527/28	2529/30	2531/32	2533/34	2535/36	2537/38	2539/40	2541/42	2543/44	2545/46	2547/48	2549/50	2551/52	2553/54	2555/56	2557/58	2559/60	2561/62	2563/64	2565/66	2567/68	2569/70	2571/72	2573/74	2575/76	2577/
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GENE	16011064	ALL Viruses (see bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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[illegible]

[illegible]

PC/GENE	ISOLATED	ALL Viruses (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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[illegible]

GENE	Protein	Antigen (as determined)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PV001	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 1	154-192	337-354										
PV002	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 3	2-24	331-337										
PV003	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	17-31	148-153	276-303									
PV004	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	137-144											
PV005	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	104-107											
PV006	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 57	3-36	109-116										
PV007	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 58	17-31											
PV008	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 59	126-150											
PV009	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	267-284	327-361										
PV010	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 71	301-329											
PV011	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	81-108											
PV012	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 16	64-67											
PV013	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	35-46											
PV014	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	35-102											
PV015	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	61-67											
PV016	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 50	301-329											
PV017	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	10-40											
PV018	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	10-40											
PV019	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 68	27-54											
PV020	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 35	11-41											
PV021	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 59	35-62											
PV022	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	75-102											
PV023	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 31	71-102											
PV024	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	71-102											
PV025	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	75-102											
PV026	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 41	75-102											
PV027	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	75-99											
PV028	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 51	71-102											
PV029	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	60-447											
PV030	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	411-438											
PV031	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	318-368											
PV032	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	185-147											
PV033	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	313-347											
PV034	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	11-110	184-212										
PV035	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	11-110	184-212										
PV036	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	31-60											
PV037	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	31-60											
PV038	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	10-44											
PV039	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	374-381											
PV040	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	374-381											
PV041	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	374-381											
PV042	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	10-37	113-140	534-581									
PV043	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	10-37	113-140	534-581									
PV044	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	10-37	202-216	534-581									
PV045	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	35-43	132-179										
PV046	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	35-43	132-179										
PV047	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	35-43	149-179										
PV048	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	149-179											
PV049	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	35-46											
PV050	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	37-44											
PV051	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	37-44											
PV052	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	314-351	301-333										
PV053	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	184-191	240-274										
PV054	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	225-333	301-333										
PV055	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV056	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV057	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV058	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV059	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV060	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV061	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV062	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV063	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
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PV094	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV095	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV096	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
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PV098	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV099	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											
PV100	PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 19	96-133											

ACCESSION	DESCRIPTION	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
AF011742	ALL VIRUSES (see bacteriophages)									
AF011743	PROTEIN									
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PCGENE	IPN1144	All Viruses (see header page)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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Region	Country	City	Year	Strain	Genotype	Accession	Area 1	Area 2	Area 3	Area 4	Area 5	Area 6	Area 7	Area 8	Area 9	Area 10	Area 11	Area 12	Area 13	Area 14	Area 15	Area 16	Area 17	Area 18	Area 19	Area 20	Area 21	Area 22	Area 23	Area 24	Area 25	Area 26	Area 27	Area 28	Area 29	Area 30	Area 31	Area 32	Area 33	Area 34	Area 35	Area 36	Area 37	Area 38	Area 39	Area 40	Area 41	Area 42	Area 43	Area 44	Area 45	Area 46	Area 47	Area 48	Area 49	Area 50	Area 51	Area 52	Area 53	Area 54	Area 55	Area 56	Area 57	Area 58	Area 59	Area 60	Area 61	Area 62	Area 63	Area 64	Area 65	Area 66	Area 67	Area 68	Area 69	Area 70	Area 71	Area 72	Area 73	Area 74	Area 75	Area 76	Area 77	Area 78	Area 79	Area 80	Area 81	Area 82	Area 83	Area 84	Area 85	Area 86	Area 87	Area 88	Area 89	Area 90	Area 91	Area 92	Area 93	Area 94	Area 95	Area 96	Area 97	Area 98	Area 99	Area 100	Area 101	Area 102	Area 103	Area 104	Area 105	Area 106	Area 107	Area 108	Area 109	Area 110	Area 111	Area 112	Area 113	Area 114	Area 115	Area 116	Area 117	Area 118	Area 119	Area 120	Area 121	Area 122	Area 123	Area 124	Area 125	Area 126	Area 127	Area 128	Area 129	Area 130	Area 131	Area 132	Area 133	Area 134	Area 135	Area 136	Area 137	Area 138	Area 139	Area 140	Area 141	Area 142	Area 143	Area 144	Area 145	Area 146	Area 147	Area 148	Area 149	Area 150	Area 151	Area 152	Area 153	Area 154	Area 155	Area 156	Area 157	Area 158	Area 159	Area 160	Area 161	Area 162	Area 163	Area 164	Area 165	Area 166	Area 167	Area 168	Area 169	Area 170	Area 171	Area 172	Area 173	Area 174	Area 175	Area 176	Area 177	Area 178	Area 179	Area 180	Area 181	Area 182	Area 183	Area 184	Area 185	Area 186	Area 187	Area 188	Area 189	Area 190	Area 191	Area 192	Area 193	Area 194	Area 195	Area 196	Area 197	Area 198	Area 199	Area 200	Area 201	Area 202	Area 203	Area 204	Area 205	Area 206	Area 207	Area 208	Area 209	Area 210	Area 211	Area 212	Area 213	Area 214	Area 215	Area 216	Area 217	Area 218	Area 219	Area 220	Area 221	Area 222	Area 223	Area 224	Area 225	Area 226	Area 227	Area 228	Area 229	Area 230	Area 231	Area 232	Area 233	Area 234	Area 235	Area 236	Area 237	Area 238	Area 239	Area 240	Area 241	Area 242	Area 243	Area 244	Area 245	Area 246	Area 247	Area 248	Area 249	Area 250	Area 251	Area 252	Area 253	Area 254	Area 255	Area 256	Area 257	Area 258	Area 259	Area 260	Area 261	Area 262	Area 263	Area 264	Area 265	Area 266	Area 267	Area 268	Area 269	Area 270	Area 271	Area 272	Area 273	Area 274	Area 275	Area 276	Area 277	Area 278	Area 279	Area 280	Area 281	Area 282	Area 283	Area 284	Area 285	Area 286	Area 287	Area 288	Area 289	Area 290	Area 291	Area 292	Area 293	Area 294	Area 295	Area 296	Area 297	Area 298	Area 299	Area 300	Area 301	Area 302	Area 303	Area 304	Area 305	Area 306	Area 307	Area 308	Area 309	Area 310	Area 311	Area 312	Area 313	Area 314	Area 315	Area 316	Area 317	Area 318	Area 319	Area 320	Area 321	Area 322	Area 323	Area 324	Area 325	Area 326	Area 327	Area 328	Area 329	Area 330	Area 331	Area 332	Area 333	Area 334	Area 335	Area 336	Area 337	Area 338	Area 339	Area 340	Area 341	Area 342	Area 343	Area 344	Area 345	Area 346	Area 347	Area 348	Area 349	Area 350	Area 351	Area 352	Area 353	Area 354	Area 355	Area 356	Area 357	Area 358	Area 359	Area 360	Area 361	Area 362	Area 363	Area 364	Area 365	Area 366	Area 367	Area 368	Area 369	Area 370	Area 371	Area 372	Area 373	Area 374	Area 375	Area 376	Area 377	Area 378	Area 379	Area 380	Area 381	Area 382	Area 383	Area 384	Area 385	Area 386	Area 387	Area 388	Area 389	Area 390	Area 391	Area 392	Area 393	Area 394	Area 395	Area 396	Area 397	Area 398	Area 399	Area 400	Area 401	Area 402	Area 403	Area 404	Area 405	Area 406	Area 407	Area 408	Area 409	Area 410	Area 411	Area 412	Area 413	Area 414	Area 415	Area 416	Area 417	Area 418	Area 419	Area 420	Area 421	Area 422	Area 423	Area 424	Area 425	Area 426	Area 427	Area 428	Area 429	Area 430	Area 431	Area 432	Area 433	Area 434	Area 435	Area 436	Area 437	Area 438	Area 439	Area 440	Area 441	Area 442	Area 443	Area 444	Area 445	Area 446	Area 447	Area 448	Area 449	Area 450	Area 451	Area 452	Area 453	Area 454	Area 455	Area 456	Area 457	Area 458	Area 459	Area 460	Area 461	Area 462	Area 463	Area 464	Area 465	Area 466	Area 467	Area 468	Area 469	Area 470	Area 471	Area 472	Area 473	Area 474	Area 475	Area 476	Area 477	Area 478	Area 479	Area 480	Area 481	Area 482	Area 483	Area 484	Area 485	Area 486	Area 487	Area 488	Area 489	Area 490	Area 491	Area 492	Area 493	Area 494	Area 495	Area 496	Area 497	Area 498	Area 499	Area 500	Area 501	Area 502	Area 503	Area 504	Area 505	Area 506	Area 507	Area 508	Area 509	Area 510	Area 511	Area 512	Area 513	Area 514	Area 515	Area 516	Area 517	Area 518	Area 519	Area 520	Area 521	Area 522	Area 523	Area 524	Area 525	Area 526	Area 527	Area 528	Area 529	Area 530	Area 531	Area 532	Area 533	Area 534	Area 535	Area 536	Area 537	Area 538	Area 539	Area 540	Area 541	Area 542	Area 543	Area 544	Area 545	Area 546	Area 547	Area 548	Area 549	Area 550	Area 551	Area 552	Area 553	Area 554	Area 555	Area 556	Area 557	Area 558	Area 559	Area 560	Area 561	Area 562	Area 563	Area 564	Area 565	Area 566	Area 567	Area 568	Area 569	Area 570	Area 571	Area 572	Area 573	Area 574	Area 575	Area 576	Area 577	Area 578	Area 579	Area 580	Area 581	Area 582	Area 583	Area 584	Area 585	Area 586	Area 587	Area 588	Area 589	Area 590	Area 591	Area 592	Area 593	Area 594	Area 595	Area 596	Area 597	Area 598	Area 599	Area 600	Area 601	Area 602	Area 603	Area 604	Area 605	Area 606	Area 607	Area 608	Area 609	Area 610	Area 611	Area 612	Area 613	Area 614	Area 615	Area 616	Area 617	Area 618	Area 619	Area 620	Area 621	Area 622	Area 623	Area 624	Area 625	Area 626	Area 627	Area 628	Area 629	Area 630	Area 631	Area 632	Area 633	Area 634	Area 635	Area 636	Area 637	Area 638	Area 639	Area 640	Area 641	Area 642	Area 643	Area 644	Area 645	Area 646	Area 647	Area 648	Area 649	Area 650	Area 651	Area 652	Area 653	Area 654	Area 655	Area 656	Area 657	Area 658	Area 659	Area 660	Area 661	Area 662	Area 663	Area 664	Area 665	Area 666	Area 667	Area 668	Area 669	Area 670	Area 671	Area 672	Area 673	Area 674	Area 675	Area 676	Area 677	Area 678	Area 679	Area 680	Area 681	Area 682	Area 683	Area 684	Area 685	Area 686	Area 687	Area 688	Area 689	Area 690	Area 691	Area 692	Area 693	Area 694	Area 695	Area 696	Area 697	Area 698	Area 699	Area 700	Area 701	Area 702	Area 703	Area 704	Area 705	Area 706	Area 707	Area 708	Area 709	Area 710	Area 711	Area 712	Area 713	Area 714	Area 715	Area 716	Area 717	Area 718	Area 719	Area 720	Area 721	Area 722	Area 723	Area 724	Area 725	Area 726	Area 727	Area 728	Area 729	Area 730	Area 731	Area 732	Area 733	Area 734	Area 735	Area 736	Area 737	Area 738	Area 739	Area 740	Area 741	Area 742	Area 743	Area 744	Area 745	Area 746	Area 747	Area 748	Area 749	Area 750	Area 751	Area 752	Area 753	Area 754	Area 755	Area 756	Area 757	Area 758	Area 759	Area 760	Area 761	Area 762	Area 763	Area 764	Area 765	Area 766	Area 767	Area 768	Area 769	Area 770	Area 771	Area 772	Area 773	Area 774	Area 775	Area 776	Area 777	Area 778	Area 779	Area 780	Area 781	Area 782	Area 783	Area 784	Area 785	Area 786	Area 787	Area 788	Area 789	Area 790	Area 791	Area 792	Area 793	Area 794	Area 795	Area 796	Area 797	Area 798	Area 799	Area 800	Area 801	Area 802	Area 803	Area 804	Area 805	Area 806	Area 807	Area 808	Area 809	Area 810	Area 811	Area 812	Area 813	Area 814	Area 815	Area 816	Area 817	Area 818	Area 819	Area 820	Area 821	Area 822	Area 823	Area 824	Area 825	Area 826	Area 827	Area 828	Area 829	Area 830	Area 831	Area 832	Area 833	Area 834	Area 835	Area 836	Area 837	Area 838	Area 839	Area 840	Area 841	Area 842	Area 843	Area 844	Area 845	Area 846	Area 847	Area 848	Area 849	Area 850	Area 851	Area 852	Area 853	Area 854	Area 855	Area 856	Area 857	Area 858	Area 859	Area 860	Area 861	Area 862	Area 863	Area 864	Area 865	Area 866	Area 867	Area 868	Area 869	Area 870	Area 871	Area 872	Area 873	Area 874	Area 875	Area 876	Area 877	Area 878	Area 879	Area 880	Area 881	Area 882	Area 883	Area 884	Area 885	Area 886	Area 887	Area 888	Area 889	Area 890	Area 891	Area 892	Area 893	Area 894	Area 895	Area 896	Area 897	Area 898	Area 899	Area 900	Area 901	Area 902	Area 903	Area 904	Area 905	Area 906	Area 907	Area 908	Area 909	Area 910	Area 911	Area 912	Area 913	Area 914	Area 915	Area 916	Area 917	Area 918	Area 919	Area 920	Area 921	Area 922	Area 923	Area 924	Area 925	Area 926	Area 927	Area 928	Area 929	Area 930	Area 931	Area 932	Area 933	Area 934	Area 935	Area 936	Area 937	Area 938	Area 939	Area 940	Area 941	Area 942	Area 943	Area 944	Area 945	Area 946	Area 947	Area 948	Area 949	Area 950	Area 951	Area 952	Area 953	Area 954	Area 955	Area 956	Area 957	Area 958	Area 959	Area 960	Area 961	Area 962	Area 963	Area 964	Area 965	Area 966	Area 967	Area 968	Area 969	Area 970	Area 971	Area 972	Area 973	Area 974	Area 975	Area 976	Area 977	Area 978	Area 979	Area 980	Area 981	Area 982	Area 983	Area 984	Area 985	Area 986	Area 987	Area 988	Area 989	Area 990	Area 991	Area 992	Area 993	Area 994	Area 995	Area 996	Area 997	Area 998	Area 999	Area 1000
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PCGENE	1971/78-84	AD Virus (no bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCGENE	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523
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PGC#	FILE NAME	101174.d	All Viruses (no bacteriophages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PV311	ROTUS	PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 1 / STRAIN RV-5)	12-40	111-145							
PV312	ROTUS	MINOR OUTER CAPSID PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 3 / STRAIN DS1)	12-40	111-145							
PV313	ROTUS	MINOR OUTER CAPSID PROTEIN	HUMAN KOTA VIRUS (SEROTYPE 1 / STRAIN WA)	111-145								
PV314	ROTUS	MINOR OUTER CAPSID PROTEIN	RABBIT KOTA VIRUS (STRAIN ALABAMA)	111-145								
PV315	ROTUS	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 KOTA VIRUS (STRAIN SA11)	111-146								
PV316	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS	9-46								
PV317	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MATSUJAMA)	12-41								
PV318	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41								
PV319	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN ENGLIS)	9-46								
PV320	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN TEATLYN)	9-46								
PV321	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN KILIJAM)	9-46								
PV322	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BILSTOL 1)	9-46								
PV323	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MATSUJAMA VACCINE)	12-41								
PV324	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN RW)	9-41								
PV325	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN UNABE VACCINE AM9)	12-41								
PV326	MUMPS	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (TYPE 3 / STRAIN DEARJING)	26-43	71-122	127-168	222-259					
PV327	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 3 / STRAIN LANG)	4-104	100-193							
PV328	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	4-13	11-104	112-160						
PV329	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARJING)	350-384								
PV330	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARJING)	285-316								
PV331	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 3 / STRAIN DEARJING)	90-117								
PV332	MUMPS	SMALL HYDROPHOBIC PROTEIN	REOVIRUS (TYPE 1 / STRAIN LANG)	35-77								
PV333	MUMPS	SMALL HYDROPHOBIC PROTEIN	CAPTOPROTEIN (STRAINING-1)	124-158								
PV334	MUMPS	SMALL HYDROPHOBIC PROTEIN	SHOPS FIBROMA VIRUS (STRAIN KASZA)	230-277								
PV335	MUMPS	SMALL HYDROPHOBIC PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	230-290								
PV336	MUMPS	SMALL HYDROPHOBIC PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-451								
PV337	MUMPS	SMALL HYDROPHOBIC PROTEIN	HUMAN CYTOMEGALOVIRUS (TYPE 6 / STRAIN UGANDA-1102)	176-201								
PV338	MUMPS	SMALL HYDROPHOBIC PROTEIN	ICUTALURID HEAPES VIRUS 1	710-737								
PV339	MUMPS	SMALL HYDROPHOBIC PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	394-421								
PV340	MUMPS	SMALL HYDROPHOBIC PROTEIN	THEMOPROTEIN TENAX VIRUS 1 (STRAIN KRA1)	169-196								
PV341	MUMPS	SMALL HYDROPHOBIC PROTEIN	THEMOPROTEIN TENAX VIRUS 1 (STRAIN KRA1)	169-196								
PV342	MUMPS	SMALL HYDROPHOBIC PROTEIN	HUMAN PARANFLUENZA 4A VIRUS (STRAIN TOSHIIBA)	4-18								
PV343	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	35-45								
PV344	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-41								
PV345	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	30-78								
PV346	MUMPS	SMALL HYDROPHOBIC PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	53-87								
PV347	MUMPS	SMALL HYDROPHOBIC PROTEIN	AUTOGRAFA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	85-112								
PV348	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	35-46								
PV349	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39								
PV350	MUMPS	SMALL HYDROPHOBIC PROTEIN	AUTOGRAFA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	80-107								
PV351	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	77-111								
PV352	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	119-153							
PV353	MUMPS	SMALL HYDROPHOBIC PROTEIN	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	14-41								
PV354	MUMPS	SMALL HYDROPHOBIC PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	14-41								
PV355	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103								
PV356	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	95-164								
PV357	MUMPS	SMALL HYDROPHOBIC PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	118-148								
PV358	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	24-37								
PV359	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	232-369								
PV360	MUMPS	SMALL HYDROPHOBIC PROTEIN	AUTOGRAFA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	133-184								
PV361	MUMPS	SMALL HYDROPHOBIC PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-149								
PV362	MUMPS	SMALL HYDROPHOBIC PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	122-149								
PV363	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	58-94								
PV364	MUMPS	SMALL HYDROPHOBIC PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	81-131	346-373	658-700						
PV365	MUMPS	SMALL HYDROPHOBIC PROTEIN	SOYBEAN CHLOROTIC MOTTLE VIRUS	13-40								
PV366	MUMPS	SMALL HYDROPHOBIC PROTEIN	FOWL POX VIRUS (ISOLATE HP-411) (MUNICH)	14-108								
PV367	MUMPS	SMALL HYDROPHOBIC PROTEIN	FOWL POX VIRUS (ISOLATE HP-411) (MUNICH)	62-89	132-179	184-218						
PV368	MUMPS	SMALL HYDROPHOBIC PROTEIN	FOWL POX VIRUS (ISOLATE HP-411) (MUNICH)	162-197	214-241							

SCHEME	GENE	10711754	ALL Viruses (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PROTEIN	POWPOX VIRUS (ISOLATE HP-43) (MUNICH)	11-18										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		121-167										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		17-116										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		161-188										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		32-43										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		53-43										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		6-35										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		170-204										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		37-44	95-126									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		31-38	179-206									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		19-53										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		47-56										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		27-54										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		94-143										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		33-76										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		64-84										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		83-89										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		92-119										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		13-42										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		5-31										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		4-40										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		44-71										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		44-71										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		59-101	106-157									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		31-101	106-157									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		56-107	197-231									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		56-107	197-231									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		44-71										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		323-333										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		116-155										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		5-32	35-96									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		204-235										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		233-237	268-399									
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		141-148										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		404-441										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		10-43										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		7-34										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		81-112										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		26-77										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		46-77										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		26-50										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		10-44										
POWPOX VIRUS (ISOLATE HP-43) (MUNICH)		132-179										

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

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PCCLONE	PROTEIN	CD	Accession (see last paragraph)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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Accession Number	Protein Name	Gene Name	Organism	Accession Number	Protein Name	Gene Name	Organism	Accession Number	Protein Name	Gene Name	Organism	Accession Number	Protein Name	Gene Name	Organism	Accession Number	Protein Name	Gene Name	Organism
P00001	Protein A	SPA	Staphylococcus aureus	P00002	Protein B	SPB	Staphylococcus aureus	P00003	Protein C	SPC	Staphylococcus aureus	P00004	Protein D	SPD	Staphylococcus aureus	P00005	Protein E	SPE	Staphylococcus aureus
P00006	Protein F	SPF	Staphylococcus aureus	P00007	Protein G	SPG	Staphylococcus aureus	P00008	Protein H	SPH	Staphylococcus aureus	P00009	Protein I	SPI	Staphylococcus aureus	P00010	Protein J	SPJ	Staphylococcus aureus
P00011	Protein K	SPK	Staphylococcus aureus	P00012	Protein L	SPL	Staphylococcus aureus	P00013	Protein M	SPM	Staphylococcus aureus	P00014	Protein N	SPN	Staphylococcus aureus	P00015	Protein O	SPO	Staphylococcus aureus
P00016	Protein P	SPP	Staphylococcus aureus	P00017	Protein Q	SPQ	Staphylococcus aureus	P00018	Protein R	SPR	Staphylococcus aureus	P00019	Protein S	SPS	Staphylococcus aureus	P00020	Protein T	SPT	Staphylococcus aureus
P00021	Protein U	SPU	Staphylococcus aureus	P00022	Protein V	SPV	Staphylococcus aureus	P00023	Protein W	SPW	Staphylococcus aureus	P00024	Protein X	SPX	Staphylococcus aureus	P00025	Protein Y	SPY	Staphylococcus aureus
P00026	Protein Z	SPZ	Staphylococcus aureus	P00027	Protein AA	SPA	Staphylococcus aureus	P00028	Protein AB	SPB	Staphylococcus aureus	P00029	Protein AC	SPC	Staphylococcus aureus	P00030	Protein AD	SPD	Staphylococcus aureus
P00031	Protein AE	SPAE	Staphylococcus aureus	P00032	Protein AF	SPAF	Staphylococcus aureus	P00033	Protein AG	SPAG	Staphylococcus aureus	P00034	Protein AH	SPAH	Staphylococcus aureus	P00035	Protein AI	SPAI	Staphylococcus aureus
P00036	Protein AJ	SPAJ	Staphylococcus aureus	P00037	Protein AK	SPAK	Staphylococcus aureus	P00038	Protein AL	SPAL	Staphylococcus aureus	P00039	Protein AM	SPAM	Staphylococcus aureus	P00040	Protein AN	SPAN	Staphylococcus aureus
P00041	Protein AO	SPAO	Staphylococcus aureus	P00042	Protein AP	SPAP	Staphylococcus aureus	P00043	Protein AQ	SPAQ	Staphylococcus aureus	P00044	Protein AR	SPAR	Staphylococcus aureus	P00045	Protein AS	SPAS	Staphylococcus aureus
P00046	Protein AT	SPAT	Staphylococcus aureus	P00047	Protein AU	SPAU	Staphylococcus aureus	P00048	Protein AV	SPAV	Staphylococcus aureus	P00049	Protein AW	SPAW	Staphylococcus aureus	P00050	Protein AX	SPAX	Staphylococcus aureus
P00051	Protein AY	SPAY	Staphylococcus aureus	P00052	Protein AZ	SPAZ	Staphylococcus aureus	P00053	Protein BA	SPBA	Staphylococcus aureus	P00054	Protein BB	SPBB	Staphylococcus aureus	P00055	Protein BC	SPBC	Staphylococcus aureus
P00056	Protein BD	SPBD	Staphylococcus aureus	P00057	Protein BE	SPBE	Staphylococcus aureus	P00058	Protein BF	SPBF	Staphylococcus aureus	P00059	Protein BG	SPBG	Staphylococcus aureus	P00060	Protein BH	SPBH	Staphylococcus aureus
P00061	Protein BI	SPBI	Staphylococcus aureus	P00062	Protein BJ	SPBJ	Staphylococcus aureus	P00063	Protein BK	SPBK	Staphylococcus aureus	P00064	Protein BL	SPBL	Staphylococcus aureus	P00065	Protein BM	SPBM	Staphylococcus aureus
P00066	Protein BN	SPBN	Staphylococcus aureus	P00067	Protein BO	SPBO	Staphylococcus aureus	P00068	Protein BP	SPBP	Staphylococcus aureus	P00069	Protein BQ	SPBQ	Staphylococcus aureus	P00070	Protein BR	SPBR	Staphylococcus aureus
P00071	Protein BS	SPBS	Staphylococcus aureus	P00072	Protein BT	SPBT	Staphylococcus aureus	P00073	Protein BU	SPBU	Staphylococcus aureus	P00074	Protein BV	SPBV	Staphylococcus aureus	P00075	Protein BW	SPBW	Staphylococcus aureus
P00076	Protein BX	SPBX	Staphylococcus aureus	P00077	Protein BY	SPBY	Staphylococcus aureus	P00078	Protein BZ	SPBZ	Staphylococcus aureus	P00079	Protein CA	SPCA	Staphylococcus aureus	P00080	Protein CB	SPCB	Staphylococcus aureus
P00081	Protein CC	SPCC	Staphylococcus aureus	P00082	Protein CD	SPCD	Staphylococcus aureus	P00083	Protein CE	SPCE	Staphylococcus aureus	P00084	Protein CF	SPCF	Staphylococcus aureus	P00085	Protein CG	SPCG	Staphylococcus aureus
P00086	Protein CH	SPCH	Staphylococcus aureus	P00087	Protein CI	SPCI	Staphylococcus aureus	P00088	Protein CJ	SPCJ	Staphylococcus aureus	P00089	Protein CK	SPCK	Staphylococcus aureus	P00090	Protein CL	SPCL	Staphylococcus aureus
P00091	Protein CM	SPCM	Staphylococcus aureus	P00092	Protein CN	SPCN	Staphylococcus aureus												

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[illegible]

PCG CODE	INSTRUMENT	ALL VIRUSES (see Instructions, page 10)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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GENE	DESCRIPTION	Accession No.	Accession No.	Accession No.	Accession No.	Accession No.	Accession No.	Accession No.	Accession No.
PULV1	PROTEIN	U01119							
PULV2	PROTEIN	U01200							
PULV3	PROTEIN	U01201							
PULV4	PROTEIN	U01202							
PULV5	PROTEIN	U01203							
PULV6	PROTEIN	U01204							
PULV7	PROTEIN	U01205							
PULV8	PROTEIN	U01206							
PULV9	PROTEIN	U01207							
PULV10	PROTEIN	U01208							
PULV11	PROTEIN	U01209							
PULV12	PROTEIN	U01210							
PULV13	PROTEIN	U01211							
PULV14	PROTEIN	U01212							
PULV15	PROTEIN	U01213							
PULV16	PROTEIN	U01214							
PULV17	PROTEIN	U01215							
PULV18	PROTEIN	U01216							
PULV19	PROTEIN	U01217							
PULV20	PROTEIN	U01218							
PULV21	PROTEIN	U01219							
PULV22	PROTEIN	U01220							
PULV23	PROTEIN	U01221							
PULV24	PROTEIN	U01222							
PULV25	PROTEIN	U01223							
PULV26	PROTEIN	U01224							
PULV27	PROTEIN	U01225							
PULV28	PROTEIN	U01226							
PULV29	PROTEIN	U01227							
PULV30	PROTEIN	U01228							
PULV31	PROTEIN	U01229							
PULV32	PROTEIN	U01230							
PULV33	PROTEIN	U01231							
PULV34	PROTEIN	U01232							
PULV35	PROTEIN	U01233							
PULV36	PROTEIN	U01234							
PULV37	PROTEIN	U01235							
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PULV47	PROTEIN	U01245							
PULV48	PROTEIN	U01246							
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PULV57	PROTEIN	U01255							
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PULV59	PROTEIN	U01257							
PULV60	PROTEIN	U01258							
PULV61	PROTEIN	U01259							
PULV62	PROTEIN	U01260							
PULV63	PROTEIN	U01261							
PULV64	PROTEIN	U01262							
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PULV70	PROTEIN	U01268							
PULV71	PROTEIN	U01269							
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PULV73	PROTEIN	U01271							
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PULV77	PROTEIN	U01275							
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PULV81	PROTEIN	U01279							
PULV82	PROTEIN	U01280							
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PULV84	PROTEIN	U01282							
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PULV92	PROTEIN	U01290							
PULV93	PROTEIN	U01291							
PULV94	PROTEIN	U01292							
PULV95	PROTEIN	U01293							
PULV96	PROTEIN	U01294							
PULV97	PROTEIN	U01295							
PULV98	PROTEIN	U01296							
PULV99	PROTEIN	U01297							
PULV100	PROTEIN	U01298							

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

[illegible]

[illegible]

[illegible]

PCGENE	107n172a4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROJLIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PATPD SYN01	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	100-137							
PATPD SYN02	ATP SYNTHASE DELTA CHAIN	SYNECHOCOCCUS SP	112-147							
PATPD SYN03	ATP SYNTHASE DELTA CHAIN	VIBRIO ALGINOLYTICUS	316-337							
PATPD SYN04	ATP SYNTHASE DELTA CHAIN	BACILLUS FIRMIUS	33-40							
PATPD SYN05	ATP SYNTHASE EPSILON CHAIN	MYCOPLASMA GALLISEPTICUM	99-126							
PATPD SYN06	ATP SYNTHASE EPSILON CHAIN	PROPIONIGENIUM MODESTUM	100-137							
PATPD SYN07	ATP SYNTHASE EPSILON CHAIN	SYNECHOCOCCUS SP	22-104							
PATPD SYN08	ATP SYNTHASE B CHAIN	ANABAENA SP	17-44	137-164						
PATPD SYN09	ATP SYNTHASE B CHAIN	BACILLUS FIRMIUS	110-151							
PATPD SYN10	ATP SYNTHASE B CHAIN	BACILLUS MEGATERIUM	33-43	172-170						
PATPD SYN11	ATP SYNTHASE B CHAIN	MYCOPLASMA GALLISEPTICUM	82-115	110-197						
PATPD SYN12	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	15-48	111-159						
PATPD SYN13	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	12-39	128-155						
PATPD SYN14	ATP SYNTHASE B CHAIN	THEMOPHILIC BACTERIUM PE-3	50-77							
PATPD SYN15	ATP SYNTHASE B CHAIN	ANABAENA SP	276-310							
PATPD SYN16	ATP SYNTHASE GAMMA CHAIN	ESCHERICHIA COLI	331-333							
PATPD SYN17	ATP SYNTHASE GAMMA CHAIN	MYCOPLASMA GALLISEPTICUM	31-43	91-140						
PATPD SYN18	ATP SYNTHASE GAMMA CHAIN	RHODOSPIRILLUM RUBRUM	210-297							
PATPD SYN19	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	280-307							
PATPD SYN20	ATP SYNTHASE GAMMA CHAIN	SYNECHOCOCCUS SP	96-126	210-207						
PATPD SYN21	ATP SYNTHASE GAMMA CHAIN	MYCOPLASMA GALLISEPTICUM	131-167							
PATPD SYN22	ATP SYNTHASE PROTEIN I	ANABAENA SP	120-158							
PATPD SYN23	ATP SYNTHASE BETA CHAIN	BACILLUS FIRMIUS	182-189	156-183						
PATPD SYN24	ATP SYNTHASE BETA CHAIN	RHODOSPIRILLUM RUBRUM	40-74							
PATPD SYN25	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	37-110	128-155						
PATPD SYN26	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	70-100							
PATPD SYN27	ATP SYNTHASE B CHAIN	SYNECHOCOCCUS SP	108-133							
PATPD SYN28	ATP SYNTHASE B CHAIN	BACILLUS MEGATERIUM	14-42							
PATPD SYN29	ATP SYNTHASE PROTEIN I	SYNECHOCOCCUS SP	90-131							
PATPD SYN30	ATP SYNTHASE PROTEIN I	PEUDOMONAS SYRINGAE	184-211	231-260						
PATPD SYN31	ATP SYNTHASE PROTEIN I	EUBACTERIUM SP	26-53							
PATPD SYN32	ATP SYNTHASE PROTEIN I	EUBACTERIUM SP	26-53							
PATPD SYN33	ATP SYNTHASE PROTEIN I	HALOBACTERIUM SP	145-176							
PATPD SYN34	ATP SYNTHASE PROTEIN I	HALOBACTERIUM SP	180-214							
PATPD SYN35	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	152-166							
PATPD SYN36	ATP SYNTHASE PROTEIN I	SYNECHOCOCCUS AGALACTICAE	92-119	138-204	367-306	141-385	417-524	542-589	1014-1041	
PATPD SYN37	ATP SYNTHASE PROTEIN I	VITREOSCILLA SP	119-148							
PATPD SYN38	ATP SYNTHASE PROTEIN I	EUBACTERIUM SP	427-450							
PATPD SYN39	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	334-361	435-455						
PATPD SYN40	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	123-154							
PATPD SYN41	ATP SYNTHASE PROTEIN I	HALOBACTERIUM HALOBUTUM	408-442							
PATPD SYN42	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	21-44							
PATPD SYN43	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	6-35							
PATPD SYN44	ATP SYNTHASE PROTEIN I	RHODOBACTER CAPSULATUS	1000-1022							
PATPD SYN45	ATP SYNTHASE PROTEIN I	RHODOBACTER CAPSULATUS	249-276							
PATPD SYN46	ATP SYNTHASE PROTEIN I	CLOSTRIDIUM PERFRINGENS	72-99	551-646						
PATPD SYN47	ATP SYNTHASE PROTEIN I	PROSTHECOCHLORIS AESTUARII	61-93							
PATPD SYN48	ATP SYNTHASE PROTEIN I	ACETOBACTER XYLINUM	111-138	1031-1082						
PATPD SYN49	ATP SYNTHASE PROTEIN I	ACETOBACTER XYLINUM	10-37							
PATPD SYN50	ATP SYNTHASE PROTEIN I	ACETOBACTER CALCOACEUS	190-217							
PATPD SYN51	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	243-270							
PATPD SYN52	ATP SYNTHASE PROTEIN I	HAEMOPHILUS INFLUENZAE	21-50							
PATPD SYN53	ATP SYNTHASE PROTEIN I	HAEMOPHILUS INFLUENZAE	157-184	236-233						
PATPD SYN54	ATP SYNTHASE PROTEIN I	HAEMOPHILUS INFLUENZAE	205-239							
PATPD SYN55	ATP SYNTHASE PROTEIN I	HAEMOPHILUS INFLUENZAE	4-33							
PATPD SYN56	ATP SYNTHASE PROTEIN I	RHODOBACTER WINGOARDII	915-953							
PATPD SYN57	ATP SYNTHASE PROTEIN I	ESCHERICHIA COLI	599-633							
PATPD SYN58	ATP SYNTHASE PROTEIN I	BACILLUS STEAROTHEROPHILUS								

ACCENSE	19741784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ZILK NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROAL CLOAB	BETA-GALACTOSIDASE	CLOSTRIDIUM ACETIBUTYLICUM	124-131								
PROAL CLOTU	BETA-GALACTOSIDASE	CLOSTRIDIUM THERMOSULFURICUM	161-191								
PROAL KLEPM	BETA-GALACTOSIDASE	KLEBSIELLA PNEUMONIAE	203-272								
PROAL LACDE	BETA-GALACTOSIDASE	LACTOBACILLUS DELBRUECKII	203-232								
PROAL STTRK	BETA-GALACTOSIDASE	STREPTOCOCCUS THERMOPHILUS	184-215								
PROAL SULSO	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	19-26	179-206							
PROAM TULIA	BETA-GALACTOSIDASE SMALL SUBUNIT	LEUCOSINOTOC LACTIS	129-156								
PROAM SULSO	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	106-140								
PROAM CLOTU	BETA-GALACTOSIDASE A	CLOSTRIDIUM THERMOSULFURICUM	333-380	418-445							
PROGLA CLOTU	BETA-GLUCOSIDASE D	CLOSTRIDIUM THERMOCELLUM	339-386	373-409	534-581	631-665					
PROGLA CLOTU	THEMOSTABLE BETA-GLUCOSIDASE	ESCHERICHIA COLI	464-494	536-563							
PROGLA ECOLI	BETA-GLUCOSIDASE	AGROMONAS THERMOPHILA	421-448								
PROGLA GASP	BETA-GLUCOSIDASE	BUTYRIVIBRIO FIBROSOLVENS	84-113	431-463	692-719	718-765					
PROGLA BUTIT	POTENTIAL DHA-INVERTASE A	STAPHYLOCOCCUS AUREUS	60-17								
PROGLA STAAU	POTENTIAL DHA-INVERTASE BINO	STAPHYLOCOCCUS AUREUS	163-197								
PROGLA STAAU	DHA-INVERTASE BINO	STAPHYLOCOCCUS AUREUS	103-190								
PROGLA BACSH	AMINO-TRANSFERASE	STAPHYLOCOCCUS AUREUS	145-172								
PROGLA BACSH	BIOTIN SYNTHETASE	BACILLUS SPHAERICUS	32-60								
PROGLA ECOLI	BIOTIN SYNTHETASE	ESCHERICHIA COLI	130-157								
PROGLA BACSH	BIOTIN SYNTHETASE	BACILLUS SPHAERICUS	144-171								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CEREUS	97-118	313-303							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE II	HAEMOPHILUS INFLUENZAE	132-139	204-231							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CEREUS	14-67	201-228							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CEREUS	14-67	201-228							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE III	BACILLUS CEREUS	33-83	95-119							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE III	PSEUDOMONAS AERUGINOSA	18-50	200-227							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CEREUS	30-66	200-227							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE II	BACTEROIDES FRAGILIS	22-49	276-307							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CEREUS	93-120	276-307							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BACILLUS LICHNERFORMIS	67-74	166-115							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PROTEUS MIRABILIS	191-231								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PROTEUS VULGARIS	4-38	240-267							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	STREPTOMYCES ALBUS O	41-70								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	KLAYSIELLA PNEUMONIAE	121-148								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	STAPHYLOCOCCUS AUREUS	19-74	99-126							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	ESCHERICHIA COLI	118-146	313-263							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	ESCHERICHIA COLI	135-196								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BACILLUS LICHNERFORMIS	129-156	514-532							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	STAPHYLOCOCCUS AUREUS	87-114	122-161	201-212	303-339					
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	TRIPONEMA PALLIDUM	312-346								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BACILLUS SUBTILIS	312-346								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PSEUDOMONAS PUTIDA	16-47								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PSEUDOMONAS PUTIDA	119-153								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PSEUDOMONAS PUTIDA	179-213								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	DESULFOTOLUBUS AMBIVALENS	157-217	342-390	381-425	343-375					
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PSEUDOMONAS AERUGINOSA	360-387	313-340							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	PSEUDOMONAS AERUGINOSA	384-421								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	ESCHERICHIA COLI	419-466								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	ESCHERICHIA COLI	6-33								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BORDETELLA PERTUSSIS	174-205								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BORDETELLA PERTUSSIS	116-143								
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BORDETELLA PERTUSSIS	39-46	202-229							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BORDETELLA PERTUSSIS	113-143	301-331							
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	BORDETELLA PERTUSSIS	312-340	666-729	815-842	851-893	941-993	1118-1207			
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	CLOSTRIDIUM BOTULINUM	666-693	725-763	802-833	833-890	1064-1091	1094-1099			
PROGLA BACSH	BETA-LACTAMASE PRECURSOR	CLOSTRIDIUM BOTULINUM	666-693	725-763	802-833	833-890	1064-1091	1094-1099			

PCGENE	18713724	Prokaryotic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PC01 CLOBO	BOTULINUM NEUROTOXIN TYPE C1 PRECURSOR	CLOSTRIDIUM BOTULINUM	84-117	114-241	720-773	798-825	850-892			
PC02 CLOBO	BOTULINUM NEUROTOXIN TYPE D PRECURSOR	CLOSTRIDIUM BOTULINUM	471-500	526-576	727-770	804-831	847-892	906-963	1040-1087	
PC03 CLOBO	BOTULINUM NEUROTOXIN TYPE E PRECURSOR	CLOSTRIDIUM BOTULINUM	314-291	350-381	704-753	773-811	890-917	992-1019	1112-1149	
PC04 CLOBO	BOTULINUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	314-291	350-381	704-753	773-811	890-917	992-1019	1112-1149	
PC05 CLOBO	BOTULINUM NEUROTOXIN TYPE F PRECURSOR	CLOSTRIDIUM BOTULINUM	649-710	753-772	892-919	1012-1040	1093-1122	1103-1210		
PC06 MICAB	CYTOKROME C150	MICROCISTIS AERUGINOSA	3-30							
PC07 BACFI	PROBABLE CADMIUM-TRANSPORTING ATPASE	BACILLUS FIRMUS	30-37	100-131	165-192	276-308	331-367			
PC08 STAAL	PROBABLE CADMIUM-TRANSPORTING ATPASE	STAPHYLOCOCCUS AUREUS	312-309	378-570						
PC09 ECOLI	TRANSCRIPTIONAL ACTIVATOR CADC	ESCHERICHIA COLI	34-45	472-443						
PC10 YEAPF	F1 CAPSULE ANCHORING PROTEIN PRECURSOR	YERSINIA PESTIS	203-240	478-437	520-537	619-646				
PC11 BACAN	CAPA PROTEIN	BACILLUS ANTHRACIS	108-118							
PC12 BACAN	CAPA PROTEIN	BACILLUS ANTHRACIS	14-70							
PC13 ANAN	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANACISTIS NIDULANS	248-293							
PC14 ANAN	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANABAENA SP	98-125	157-164	687-728					
PC15 CORGL	PHOSPHOENOLPYRUVATE CARBOXYLASE	CORYNEBACTERIUM GLUTAMICUM	13-42							
PC16 ECOLI	PHOSPHOENOLPYRUVATE CARBOXYLASE	ESCHERICHIA COLI	33-62							
PC17 BACSU	CARBAMOYL-PHOSPHATE SYNTHETASE	BACILLUS SUBTILIS	370-319							
PC18 BACSU	CARBAMOYL-PHOSPHATE SYNTHETASE	BACILLUS SUBTILIS	706-631							
PC19 ECOLI	CARBAMOYL-PHOSPHATE SYNTHETASE LARGE CHAI	ESCHERICHIA COLI	450-481							
PC20 STAAL	CHOLERAEPHICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	7-34	87-114						
PC21 STAAL	CHOLERAEPHICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	3-34	87-114						
PC22 AGCA	CATECHOL 1,2-DIOXYGENASE	ACINETOBACTER CALCOACETICUS	31-45							
PC23 BACST	PEROXIDASE / CATALASE	BACILLUS STEAROTHERIOPHILUS	440-470							
PC24 ECOLI	CATALASE HPI	ESCHERICHIA COLI	379-406							
PC25 ECOLI	CATALASE	MICROCOCCUS LUTEUS	431-480							
PC26 BACLI	CATALASE HPI	SALMONELLA PYRUMINUMI	111-142	140-407						
PC27 BACLI	CATALASE HPI	ESCHERICHIA COLI	111-142							
PC28 ECOLI	CHOLERAEPHICOL ACETYLTRANSFERASE	CAMPYLOBACTER COLI	84-111							
PC29 ECOLI	CHOLERAEPHICOL ACETYLTRANSFERASE	CLOSTRIDIUM BUTYRICUM	98-115							
PC30 ECOLI	CHOLERAEPHICOL ACETYLTRANSFERASE	ESCHERICHIA COLI	92-119							
PC31 BACSU	CHOLERAEPHICOL ACETYLTRANSFERASE	PROTEUS MIRABILIS	92-119							
PC32 STAAL	CHOLERAEPHICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS INTERMEDIUS	3-34	87-114						
PC33 STAAL	CHOLERAEPHICOL ACETYLTRANSFERASE	STAPHYLOCOCCUS AGALACTIAE	3-34	87-114						
PC34 ECOLI	CHOLERAEPHICOL ACETYLTRANSFERASE	COXIELLA BURNETII	106-276							
PC35 THIVU	CARBOXYPEPTIDASE Y PRECURSOR	THEMACTINOMYCES VULGARIS	48-75							
PC36 ECOLI	TRNA NUCLEOTIDYLTRANSFERASE	ESCHERICHIA COLI	76-403							
PC37 ECOLI	TRNA NUCLEOTIDYLTRANSFERASE	SYNECHOCOCCUS SP	36-56							
PC38 SYNPP	COI CONC MECH PROTEIN CDOR	SYNECHOCOCCUS SP	217-236	331-372	445-486					
PC39 THET	CYCLOMAL TOXESTRINASE	THERMOANEROBACTER ETILANOLICUS	301-332							
PC40 BACDA	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS MACERANS	439-466	616-643						
PC41 BACDA	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS MACERANS	210-251	416-466	615-642					
PC42 BACCI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS CIRCULANS	217-244	442-472	594-631					
PC43 BACCI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS LICHENIFORMIS	217-244	442-472	594-647					
PC44 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS OHBENSIS	470-471							
PC45 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-463	615-642					
PC46 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	409-431							
PC47 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-463	615-642					
PC48 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	210-237	433-463	615-642					
PC49 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	217-244	442-472	594-631					
PC50 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS SP	586-644							
PC51 BACSU	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	BACILLUS STEAROTHERIOPHILUS	212-239							
PC52 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	KLEBSIELLA PNEUMONIAE	44-71	283-326						
PC53 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	44-71	283-326						
PC54 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	SHIGELLA SONNEI	44-71	283-326						
PC55 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC56 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC57 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC58 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC59 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC60 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC61 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC62 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC63 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC64 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC65 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC66 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC67 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC68 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC69 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC70 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC71 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC72 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC73 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC74 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC75 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC76 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC77 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC78 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC79 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC80 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC81 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC82 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC83 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC84 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC85 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC86 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC87 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC88 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC89 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC90 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC91 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC92 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC93 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC94 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC95 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC96 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC97 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC98 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC99 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							
PC100 ECOLI	CYCLOMAL TOXEST GLUCANOTRANS PRECURSOR	ESCHERICHIA COLI	314-368							

PCGENE	(1071) Field	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5
FILE NAME	PROTEIN	ORGANISM	384-311				
PC001	COLICIN D	ESCHERICHIA COLI	176-237				
PC002	COLICIN M	ESCHERICHIA COLI	116-146				
PC003	COLICIN N	ESCHERICHIA COLI	318-331				
PC004	COLICIN A	CITROBACTER FREUNDII	370-397				
PC005	ISOPENTICLIN HEPHEDASE	STREPTOMYCES CLAVULIGERUS	61-93	315-312	378-412	413-432	
PC006	COLICIN B	ESCHERICHIA COLI	68-93	315-312	378-412	413-432	
PC007	COLICIN E	ESCHERICHIA COLI	39-49				
PC008	COLICIN B	ESCHERICHIA COLI	76-103				
PC009	COLICIN B	ESCHERICHIA COLI	37-53				
PC010	COLICIN B	ESCHERICHIA COLI	138-187	318-416	361-395		
PC011	COLICIN B	ESCHERICHIA COLI	131-160				
PC012	COLICIN B	ESCHERICHIA COLI	180-203	244-271			
PC013	COLICIN B	ESCHERICHIA COLI	57-93				
PC014	COLICIN B	ESCHERICHIA COLI	64-93				
PC015	COLICIN B	ESCHERICHIA COLI	57-84				
PC016	COLICIN B	ESCHERICHIA COLI	64-93				
PC017	COLICIN B	ESCHERICHIA COLI	57-84				
PC018	COLICIN B	ESCHERICHIA COLI	61-92				
PC019	COLICIN B	ESCHERICHIA COLI	64-93				
PC020	COLICIN B	ESCHERICHIA COLI	141-181	319-370	421-466		
PC021	COLICIN B	ESCHERICHIA COLI	117-163				
PC022	COLICIN B	ESCHERICHIA COLI	299-333				
PC023	COLICIN B	ESCHERICHIA COLI	398-333	337-364			
PC024	COLICIN B	ESCHERICHIA COLI	131-163	398-368			
PC025	COLICIN B	ESCHERICHIA COLI	117-144	378-366			
PC026	COLICIN B	ESCHERICHIA COLI	4-31				
PC027	COLICIN B	ESCHERICHIA COLI	4-31				
PC028	COLICIN B	ESCHERICHIA COLI	300-327				
PC029	COLICIN B	ESCHERICHIA COLI	318-333	337-364	451-483		
PC030	COLICIN B	ESCHERICHIA COLI	337-368	411-444			
PC031	COLICIN B	ESCHERICHIA COLI	300-337	348-381			
PC032	COLICIN B	ESCHERICHIA COLI	338-366	417-444			
PC033	COLICIN B	ESCHERICHIA COLI	299-333				
PC034	COLICIN B	ESCHERICHIA COLI	298-332	432-479			
PC035	COLICIN B	ESCHERICHIA COLI	331-352	316-363	317-364		
PC036	COLICIN B	ESCHERICHIA COLI	123-152	371-364			
PC037	COLICIN B	ESCHERICHIA COLI	338-366				
PC038	COLICIN B	ESCHERICHIA COLI	117-163	322-370	423-466		
PC039	COLICIN B	ESCHERICHIA COLI	101-130	393-316	360-394		
PC040	COLICIN B	ESCHERICHIA COLI	308-333	371-380			
PC041	COLICIN B	ESCHERICHIA COLI	338-363	451-489			
PC042	COLICIN B	ESCHERICHIA COLI	377-384				
PC043	COLICIN B	ESCHERICHIA COLI	116-148	337-364			
PC044	COLICIN B	ESCHERICHIA COLI	371-400	393-399			
PC045	COLICIN B	ESCHERICHIA COLI	316-386	590-617			
PC046	COLICIN B	ESCHERICHIA COLI	162-191				
PC047	COLICIN B	ESCHERICHIA COLI	124-151				
PC048	COLICIN B	ESCHERICHIA COLI	68-113				
PC049	COLICIN B	ESCHERICHIA COLI	88-115				
PC050	COLICIN B	ESCHERICHIA COLI	22-49				
PC051	COLICIN B	ESCHERICHIA COLI	32-49				
PC052	COLICIN B	ESCHERICHIA COLI	491-318	366-393			
PC053	COLICIN B	ESCHERICHIA COLI	145-372				
PC054	COLICIN B	ESCHERICHIA COLI	166-371				

[illegible]

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EC-GENE	1975-1984	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PROTEIN		ORGANISM							
GLUCOSE 1-DEHYDROGENASE B		BACILLUS MEGATERIUM	27-37						AREA2
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	436-463						
GLUCOSE DEHYDROGENASE		STREPTOMYCES VIOLACEORUBER	108-195						
GLUCOSE DEHYDROGENASE		BACILLUS STEAROTHERMOPHILUS	192-219						
GLUCOSE DEHYDROGENASE		AGROBACTERIUM TUMEFACIENS	117-244						
GLUCOSE DEHYDROGENASE		METHYLOBACTERIUM EXTOLOENS	132-187		190-224				
GLUCOSE DEHYDROGENASE		METHYLOBACTERIUM ORGANOPHILUM	132-187		190-224				
GLUCOSE DEHYDROGENASE		PARACOCCLUS DENTIFICANS	191-232						
GLUCOSE DEHYDROGENASE		BACILLUS SP	242-314						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	180-214						
GLUCOSE DEHYDROGENASE		BACILLUS SUBTILIS	72-107		406-433				
GLUCOSE DEHYDROGENASE		CONTRIBUTUM CLUTINUM	102-132						
GLUCOSE DEHYDROGENASE		BACILLUS SPHAERICUS	312-319						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	422-512						
GLUCOSE DEHYDROGENASE		ANABENA CYLINDRICA	66-113		130-168				
GLUCOSE DEHYDROGENASE		SYNCHOCOCCLUS SP	133-168						
GLUCOSE DEHYDROGENASE		METHYLOBACTERIUM METHYLOPHILUS	419-444						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	34-43		112-141				
GLUCOSE DEHYDROGENASE		BACILLUS SUBTILIS	91-120						
GLUCOSE DEHYDROGENASE		PSEUDOMONAS PUTIDA	18-43		224-276				
GLUCOSE DEHYDROGENASE		ALZOTOBACTER VINELANDII	32-134						
GLUCOSE DEHYDROGENASE		BACILLUS STEAROTHERMOPHILUS	108-133						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	124-131		223-275				
GLUCOSE DEHYDROGENASE		PSEUDOMONAS FLUORESCENS	61-90						
GLUCOSE DEHYDROGENASE		PSEUDOMONAS PUTIDA	497-526		540-581				
GLUCOSE DEHYDROGENASE		BACILLUS SUBTILIS	436-483						
GLUCOSE DEHYDROGENASE		BACILLUS SUBTILIS	316-380						
GLUCOSE DEHYDROGENASE		BORRELLIA BURGDORFERI	182-216		341-387	436-483			
GLUCOSE DEHYDROGENASE		BUCCHERIA APUDICOLA	171-100		313-340				
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	164-400						
GLUCOSE DEHYDROGENASE		MICROCOCCUS LUTEUS	353-413						
GLUCOSE DEHYDROGENASE		MYCOPLASMA CAPRICOLUM	8-16		350-389				
GLUCOSE DEHYDROGENASE		PROTEUS MIRABILIS	383-399						
GLUCOSE DEHYDROGENASE		PSEUDOMONAS PUTIDA	308-419						
GLUCOSE DEHYDROGENASE		STREPTOMYCES	43-72		34-110	145-180			
GLUCOSE DEHYDROGENASE		CHLAMYDIA TRACHOMATIS	312-353						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	82-109						
GLUCOSE DEHYDROGENASE		SALMONELLA TYPHIMURUM	146-190						
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	487-534		548-581				
GLUCOSE DEHYDROGENASE		BACILLUS MEGATERIUM	312-394						
GLUCOSE DEHYDROGENASE		BORRELLIA BURGDORFERI	248-275		313-346				
GLUCOSE DEHYDROGENASE		BACILLUS OVIS	561-588						
GLUCOSE DEHYDROGENASE		CALDOBACTER CRESCENTUS	499-526						
GLUCOSE DEHYDROGENASE		CLOSTRIDIUM ACETOBUTYLICUM	494-537						
GLUCOSE DEHYDROGENASE		CLOSTRIDIUM PENTRUNCENS	533-539						
GLUCOSE DEHYDROGENASE		MYCOBACTERIUM TUBERCULOSIS	302-339						
GLUCOSE DEHYDROGENASE		STREPTOMYCES COELICOLOR	41-71		333-372				
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	114-141						
GLUCOSE DEHYDROGENASE		SYNCHOCOCCLUS	634-712						
GLUCOSE DEHYDROGENASE		STREPTOMYCES PELICULUS	34-51						
GLUCOSE DEHYDROGENASE		SULFOLOBUS SOLFATARICUS	104-172						
GLUCOSE DEHYDROGENASE		BACILLUS SUBTILIS	58-85		417-444				
GLUCOSE DEHYDROGENASE		ESCHERICHIA COLI	77-104						
GLUCOSE DEHYDROGENASE		SACCHAROPOLYSPOREA ERYTHRAEA	330-357						

ACCIDENT	10717814	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PROT1 BACU	DNA POLYMERASE III, ALPHA CHAIN	SALMONELLA TYPHIMURUM	171-104									
PROT2 BACU	DNA POLYMERASE III, BETA CHAIN	BACILLUS SUBTILIS	312-339									
PROT3 BACU	DNA POLYMERASE III, BETA CHAIN	BORRELIA BURGDORFERI	106-313									
PROT4 BACU	DNA POLYMERASE III, BETA CHAIN	BORRELIA AMERICANA	11-42	308-339								
PROT5 BACU	DNA POLYMERASE III, BETA CHAIN	MICROCOCCUS LUTEUS	191-218									
PROT6 BACU	DNA POLYMERASE III, BETA CHAIN	MYCOPLASMA CAPRICOLUM	14-70									
PROT7 BACU	DNA POLYMERASE III, BETA CHAIN	PSEUDOMONAS PUTIDA	10-60									
PROT8 BACU	DNA POLYMERASE III, BETA CHAIN	SPINOPHILUS CITRI	78-113	128-177	273-310							
PROT9 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	311-332									
PROT10 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	691-743									
PROT11 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	401-448									
PROT12 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS PNEUMONIAE	76-120									
PROT13 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS CALDUTENAX	208-315									
PROT14 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS PNEUMONIAE	198-225	398-433	571-598	643-672						
PROT15 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	THERMUS AQUATICUS	196-223	601-629								
PROT16 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	THERMUS AQUATICUS	597-628									
PROT17 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	169-196									
PROT18 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	MYCOCOCCUS FLAVUS	746-773									
PROT19 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SULFOLOBUS SOLFATARICUS	379-406	416-463	747-774							
PROT20 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	THERMOCOCCUS LITORALIS	332-370	551-589	692-726	1004-1031	1153-1194					
PROT21 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	LACTOCOCCUS LACTIS	716-753									
PROT22 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	LACTOCOCCUS LACTIS	716-753									
PROT23 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	4-43									
PROT24 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS EQUIMILIS	37-60	291-316								
PROT25 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS PECTINUS	284-313									
PROT26 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS AUREUS	62-89									
PROT27 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS CIRCULANS	134-161	302-339	424-451							
PROT28 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	66-98	152-185	525-552	691-723	102-116	871-905				
PROT29 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	151-178									
PROT30 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	30-47									
PROT31 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	30-47									
PROT32 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS AUREUS	32-39	118-146								
PROT33 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	DESULFOCOCCUS MOBILIS	427-481									
PROT34 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	HALOBACTERIUM HALOBILIUM	186-213									
PROT35 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	METHANOCOCCUS VANNIELII	409-436									
PROT36 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SULFOLOBUS ACIDOPHILUS	16-43	141-180								
PROT37 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	THERMOPHILUS ACIDOPHILUS	13-40	48-76	270-347							
PROT38 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ANACYSTIS NIDULANS	332-359									
PROT39 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	214-281									
PROT40 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	MYCOBACTERIUM LEPRAE	311-339	316-357								
PROT41 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SALMONELLA TYPHIMURUM	314-361									
PROT42 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SPIRILLUM PLATENSIS	314-374	481-511								
PROT43 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SYNCHOCYSTIS SP	14-41									
PROT44 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS LACTOSUS	221-238									
PROT45 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS LACTOSUS	221-238									
PROT46 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	STREPTOCOCCUS LACTOSUS	221-238									
PROT47 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	ESCHERICHIA COLI	101-113									
PROT48 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	SPINOPHILUS CITRI	27-34	134-161								
PROT49 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT50 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT51 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT52 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT53 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT54 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT55 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT56 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT57 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT58 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT59 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT60 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT61 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT62 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT63 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT64 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT65 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT66 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT67 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT68 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT69 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT70 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT71 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT72 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT73 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT74 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT75 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT76 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT77 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT78 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT79 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT80 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT81 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT82 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT83 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT84 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT85 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT86 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT87 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT88 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT89 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT90 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT91 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT92 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT93 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT94 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT95 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT96 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT97 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT98 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT99 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								
PROT100 BACU	DNA POLYMERASE III, SUBUNIT G AND TAU	BACILLUS SUBTILIS	18-45	236-236								

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PGCENE	107n17124	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PFDA1 ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	595-422									
PFDA2 ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	WOLINELLA SUCCININGENUS	487-316									
PFDA3 ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	MYXOCOCCUS XANTHUS	6-35									
PFDA4 ECOLI	GLIDING MOTILITY REGULATORY PROTEIN	CLOSTRIDIUM THERMOPHILUM	163-190									
PFDA5 ECOLI	FORMATE-TETRAHYDROFOLATE LIGASE	METHANOBACTERIUM THERMOPHILUM	76-110									
PFDA6 ECOLI	FORMATE-TETRAHYDROFOLATE LIGASE	BACILLUS SUBTILIS	301-318									
PFDA7 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	4-31									
PFDA8 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	63-90									
PFDA9 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	151-188									
PFDA10 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	278-305									
PFDA11 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	308-340									
PFDA12 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	7-43									
PFDA13 ECOLI	L-PUCOSE OPERON ACTIVATOR	BACILLUS STEAROTHERMOPHILUS	390-317									
PFDA14 ECOLI	FUMARATE HYDROLYTASE CLASS I, AEROBIC	BACILLUS SUBTILIS	414-445									
PFDA15 ECOLI	FUMARATE HYDROLYTASE	YERSINIA PESTIS	99-110									
PFDA16 ECOLI	FUMARATE HYDROLYTASE	ESCHERICHIA COLI	102-339									
PFDA17 ECOLI	GLYC-1-PHOS DEHYDROGENASE A	ANABASNA VARABILLIS	17-114									
PFDA18 ECOLI	GLYC-1-PHOS DEHYDROGENASE B	ANABASNA VARABILLIS	162-189									
PFDA19 ECOLI	GLYC-1-PHOS DEHYDROGENASE C	ESCHERICHIA COLI	236-324									
PFDA20 ECOLI	GLYC-1-PHOS DEHYDROGENASE	BACILLUS MEGATERIUM	49-76									
PFDA21 ECOLI	GLYC-1-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	49-76									
PFDA22 ECOLI	GLYC-1-PHOS DEHYDROGENASE	PYROCOCCUS WOESI	238-286									
PFDA23 ECOLI	GLYC-1-PHOS DEHYDROGENASE	THEMOTOGIA MARITIMA	390-318									
PFDA24 ECOLI	GLUCOSE-4-PHOSPHATE ISOMERASE B	BACILLUS STEAROTHERMOPHILUS	103-141									
PFDA25 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	301-328									
PFDA26 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ZYMONOMAS MOBILIS	183-192									
PFDA27 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	178-203									
PFDA28 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	84-113									
PFDA29 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	SALMONELLA TYPHIMURUM	124-158									
PFDA30 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	HABONPHILUS INFLUENZAE	394-423									
PFDA31 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	LACTOBACILLUS HELVETICUS	53-81									
PFDA32 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	SALMONELLA TYPHIMURUM	183-192									
PFDA33 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	HABONPHILUS INFLUENZAE	331-378									
PFDA34 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	78-105									
PFDA35 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	PHOTOBACTERIUM LEONINATHI	197-227									
PFDA36 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	10-37									
PFDA37 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	216-244									
PFDA38 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	60-84									
PFDA39 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	24-51									
PFDA40 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	BACILLUS SUBTILIS	293-323									
PFDA41 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	BACILLUS SUBTILIS	12-40									
PFDA42 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	STAPHYLOCOCCUS HAEMOLYTICUS	6-33									
PFDA43 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	STAPHYLOCOCCUS HAEMOLYTICUS	394-423									
PFDA44 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	331-368									
PFDA45 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	319-366									
PFDA46 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	BACILLUS SUBTILIS	34-61									
PFDA47 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	321-353									
PFDA48 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	SYNECHOCYSTIS SP	218-222									
PFDA49 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	30-79									
PFDA50 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	236-283									
PFDA51 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	114-141									
PFDA52 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	SALMONELLA TYPHIMURUM	114-141									
PFDA53 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	206-243									
PFDA54 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	METHANOCOCCUS THERMOPHILUS	58-83									

PCGENE	10/31/84	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PCGENE	10/31/84	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

PCGENE	INITIAL	Protein Name	ABU1	ABU2	ABU3	ABU4	ABU5	ABU6	ABU7
FILE NAME	PROTEIN	ORGANISM							
PGSP_XANCP	PROTEIN	XANTHOMONAS CAMPESINUS	716-117						AREA1
PGSP_PZAE	PROTEIN	XANTHOMONAS AERUGINOSA	18-39						AREA2
PGSP_AERNV	PROTEIN	XANTHOMONAS HYDROPHILA	37-41						AREA3
PGSP_EAWCA	PROTEIN	ERWINIA CAROTOVORA	15-47						AREA4
PGSP_KLEPN	PROTEIN	KLEBSIELLA PNEUMONIAE	140-167						AREA5
PGSP_EAWCA	PROTEIN	ERWINIA CAROTOVORA	28-53						AREA6
PGSP_KLEPN	PROTEIN	ERWINIA CHRYSAANTHEMI	18-53						AREA7
PGSP_PZAE	PROTEIN	KLEBSIELLA PNEUMONIAE	73-99						AREA8
PGSP_KLEPN	PROTEIN	XANTHOMONAS AERUGINOSA	54-289						AREA9
PGSP_EAWCA	PROTEIN	ERWINIA CHRYSAANTHEMI	7-42	248-216	331-338				AREA10
PGSP_XANCP	PROTEIN	XANTHOMONAS CAMPESINUS	18-73	397-334					AREA11
PGSP_EAWCA	PROTEIN	ERWINIA CAROTOVORA	108-143						AREA12
PGSP_EAWCA	PROTEIN	ERWINIA CHRYSAANTHEMI	359-103	448-413	546-573	637-688			AREA13
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS DOWNII	42-49	177-204	215-239	444-491	1463-1379		AREA14
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS DOWNII	171-198	208-211	450-485	1192-1412	1407-1574		AREA15
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS MUTANS	297-330						AREA16
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS MUTANS	42-93	110-137	161-188	199-246	313-347	392-527	AREA17
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS MUTANS	4-40	110-138	333-263	370-361	614-651		AREA18
PGSP_EAWCA	PROTEIN	STREPTOCOCCUS DOWNII	215-316	436-463	1231-1313				AREA19
PGSP_EAWCA	PROTEIN	METHANOBACTERIUM THERMOPHILICUM	80-107	148-175					AREA20
PGSP_EAWCA	PROTEIN	BACILLUS SUBTILIS	314-348	599-436	478-503				AREA21
PGSP_EAWCA	PROTEIN	ESCHERICHIA COLI	105-133						AREA22
PGSP_EAWCA	PROTEIN	BACILLUS CIRCULANS	164-191						AREA23
PGSP_EAWCA	PROTEIN	BACILLUS LICHENIFORMIS	132-166						AREA24
PGSP_EAWCA	PROTEIN	BACILLUS MACERANS	136-160						AREA25
PGSP_EAWCA	PROTEIN	BACILLUS SP	11-49						AREA26
PGSP_EAWCA	PROTEIN	BACILLUS SUBTILIS	370-304	378-403					AREA27
PGSP_EAWCA	PROTEIN	BUTYRIVIBRIO FIBRILLOLUS	134-181	432-493					AREA28
PGSP_EAWCA	PROTEIN	BACILLUS SUBTILIS	370-304						AREA29
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	201-231						AREA30
PGSP_EAWCA	PROTEIN	BACILLUS SP	116-137	148-178	538-565				AREA31
PGSP_EAWCA	PROTEIN	BACILLUS SUBTILIS	370-304						AREA32
PGSP_EAWCA	PROTEIN	FIBROBACTER SUCCINOGENES	347-386						AREA33
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	308-342						AREA34
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	44-71						AREA35
PGSP_EAWCA	PROTEIN	BACILLUS LAUTUS	410-437	454-481					AREA36
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM THERMOCELLUM	314-384						AREA37
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	762-789						AREA38
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	294-331						AREA39
PGSP_EAWCA	PROTEIN	RUMINOCOCCUS FLAVIFACIENS	376-503						AREA40
PGSP_EAWCA	PROTEIN	BACILLUS LAUTUS	331-430	444-478					AREA41
PGSP_EAWCA	PROTEIN	CALDOCCELLUM SACCHAROLYTICUM	151-182						AREA42
PGSP_EAWCA	PROTEIN	CELLULOSOMONAS FIUMI	266-293						AREA43
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM CELLULOVOLANS	144-171	266-300					AREA44
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM THERMOCELLUM	514-541						AREA45
PGSP_EAWCA	PROTEIN	CELLULOSOMONAS FIUMI	811-903						AREA46
PGSP_EAWCA	PROTEIN	THERMOPHOSPORA FUSCA	32-82						AREA47
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM CELLULOYTICUM	381-453						AREA48
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM CELLULOYTICUM	145-172	371-398					AREA49
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM THERMOCELLUM	138-183	283-316	384-311				AREA50
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM THERMOCELLUM	46-51	424-432					AREA51
PGSP_EAWCA	PROTEIN	ERWINIA CAROTOVORA	20-47	115-149					AREA52
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM THERMOCELLUM	183-139						AREA53
PGSP_EAWCA	PROTEIN	CLOSTRIDIUM STERILIS	396-236	523-546					AREA54
PGSP_EAWCA	PROTEIN	BACILLUS SP	188-235						AREA55
PGSP_EAWCA	PROTEIN	BACILLUS SP	321-348						AREA56
PGSP_EAWCA	PROTEIN	BACILLUS SP	198-239	501-521	633-664				AREA57

[illegible]

PCGENE	107s175s4	Proteotypic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462
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[illegible]

PCGENE	1971-1984	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
ADAMANTIN	ADAMANTIN	ADAMANTIN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								

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PGCENE	1071114	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
FILENAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12
PHICAB METE	METHYL-COENZYME M REDUCTASE	METHANOTREBARUS FERVIDUS	267-294											
PHICAB METVO	METHYL-COENZYME N REDUCTASE	METHANOCOCCLUS VOLTAE	247-274											
PHICAC ECOLI	MERC PROTEIN	ESCHERICHIA COLI	111-145											
PHICED METVO	REDUCTASE OPERON PROTEIN D	METHANOCOCCLUS VOLTAE	94-91											
PHIDI ECOLI	MALATE DEHYDROGENASE	ESCHERICHIA COLI	127-134											
PHIDI METE	MALATE DEHYDROGENASE	METHANOTREBARUS FERVIDUS	14-48											
PHIDI SALT	MALATE DEHYDROGENASE	SALMONELLA TYPHIMURUM	127-134											
PHID ECOLI	MDL PROTEIN	ESCHERICHIA COLI	464-491	164-711	992-1019									
PHID ECOLI	BIOGENESIS PROTEIN MDH	ESCHERICHIA COLI	119-132											
PHICI STAEF	METHICILLIN RESISTANCE PROTEIN MECI	EPIDERMIDIS A AUREUS	88-122											
PHICR STAEF	METHICILLIN RESISTANCE MECI PROTEIN	STAPHYLOCOCCUS	419-495	144-373										
PHICB METCA	METHANE MONOOXYGENASE COMPONENT A	EPIDERMIDIS A AUREUS	214-248											
PHICB METR	METHANE MONOOXYGENASE COMPONENT A	METHYLOCOCCUS CAPILLATUS	331-348											
PHICD ECOLI	SHIC SYNTHASE	METHYLOCOCCUS TRICHOSPORUM	333-367											
PHICL STALI	PROBABLE HQ TRANSPORT PROTEIN	ESCHERICHIA COLI	159-186											
PHICL BACR	MERCURIC REDUCTASE	STREPTOMYCES LIVIDANS	146-180											
PHICL STAAU	MERCURIC REDUCTASE	BACILLUS SP	392-347	132-316										
PHICR STAAU	MERCURIC RESISTANCE OPERON NEG PROTEIN	STAPHYLOCOCCUS AUREUS	16-113											
PHICB ECOLI	CYSTATHIONINE GAMMA-SYNTHASE	STAPHYLOCOCCUS AUREUS	156-183											
PHIC ECOLI	CYSTATHIONINE BETA-L YASE	ESCHERICHIA COLI	363-390											
PHIC ECOLI	CYSTATHIONINE BETA-L YASE	ESCHERICHIA COLI	2-79											
PHIC ECOLI	METHIONINE SYNTHASE	ESCHERICHIA COLI	448-482											
PHIC ECOLI	METHIONINE SYNTHASE	ESCHERICHIA COLI	371-398	642-616										
PHIC ECOLI	TRANSCRIPTION-REPAIR COUPLING FACTOR	ESCHERICHIA COLI	183-212											
PHIC ECOLI	GALACTOSIDE-BINDING PROTEIN	ESCHERICHIA COLI	82-89	312-310										
PHIC BACSU	SEPTUM SITE-DETERMINING PROTEIN MHC	ESCHERICHIA COLI	93-123											
PHIC ECOLI	MHC PROTEIN	BACILLUS SUBTILIS	102-129											
PHIC ECOLI	37 KD MEMBRANE PROTEIN PRECURSOR I	ESCHERICHIA COLI	41-71											
PHIC ECOLI	OUTER MEMBRANE PROTEIN MIP PRECURSOR	CHLAMYDIA TRACHOMATIS	106-133											
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	LEGIONELLA MICHAELIS	8-81	120-134										
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	ENTEROCOCCUS FAECALIS	4-81											
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	STAPHYLOCOCCUS AUREUS	8-87											
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	ENTEROCOCCUS FAECALIS	4-81	120-154										
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	BACTEROIDES FRAGILIS	16-41											
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	ESCHERICHIA COLI	4-81	120-154										
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	STREPTOCOCCUS PNEUMONIAE	4-81	120-154										
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	STREPTOCOCCUS SANGUIS	4-81	120-154										
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	BACTEROIDES FRAGILIS	16-41											
PHIC ECOLI	RNA ADENINE N4-METHYLTRANSFERASE	METHYLOCOCCUS CAPILLATUS	14-44											
PHIC ECOLI	METHANE MONOOXYGENASE NEG PROTEIN II	ESCHERICHIA COLI	49-76											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	THIOBACILLUS FERROOXIDANS	94-121	231-278										
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	THIOBACILLUS FERROOXIDANS	20-47											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	THIOBACILLUS FERROOXIDANS	94-132											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	ESCHERICHIA COLI	43-72											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	ESCHERICHIA COLI	241-270											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	CLOSTRIDIUM PASTEURIANUM	26-53											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	CLOSTRIDIUM PASTEURIANUM	26-44											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	PACCOCCUS DENTIFICANS	208-214	105-214										
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	SYNECHOCOCCUS SP	2-38	105-107	192-233									
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	SYNECHOCOCCUS SP	3-31	175-216										
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	ESCHERICHIA COLI	134-163											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	BACILLUS SUBTILIS	106-133											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	BACILLUS CEREUS	186-213	247-251										
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	BACILLUS SUBTILIS	63-112											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	KLASSELLA PNEUMONIAE	184-213											
PHIC ECOLI	MOLYBDOPICAC BIOSYN PROTEIN B	KLASSELLA PNEUMONIAE	53-82	433-489	193-233									

PCGENE	10/11/78-4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
ELK-NANK	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PARKO KLEPM	FUSOBACTERICUM ADIESIN PROTEIN PRECURSOR	KLEBSIELLA PNEUMONIAE	222-340							
PARKO KLEPM	MURK PROTEIN	KLEBSIELLA PNEUMONIAE	193-230							
PARKO STRYP	FIBRINOGEN / VQ-BINDING PROTEIN PRECURSOR	STREPTOCOCCUS PYOGENES	7-46	99-110						
PARKO STRYP	MURAMIDASE-RELEASED PROTEIN PRECURSOR	STREPTOCOCCUS SUI	135-102	110-177						
PARKO STRYP	PROB ATP-BINDING TRANSPORT PROTEIN MSBA	ESCHERICHIA COLI	116-150	412-449						
PARKO STRYP	EATYTHROMYCIN RESISTANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	174-223	323-350						
PARKO STRYP	ACIDIC PROTEIN MSVB	ESCHERICHIA COLI	71-100							
PARKO STRYP	MODIFICATION METHYLASE ECO171	ESCHERICHIA COLI	350-314	474-544						
PARKO STRYP	MODIFICATION METHYLASE ACC1	ACINETOBACTER CALCOACEITICUS	103-340							
PARKO STRYP	MODIFICATION METHYLASE AQU1 BETA SUBUNIT	SYNETHOCOCCLUS SP	19-46							
PARKO STRYP	MODIFICATION METHYLASE BEPI	BREVIBACTERIUM EPIDERMIDIS	166-200	309-336						
PARKO STRYP	MODIFICATION METHYLASE HGRI	HENPETOSSIPHON AURANTIACUS	281-308							
PARKO STRYP	MODIFICATION METHYLASE BAQHII	BACILLUS AMYLOLIQUEFACIENS	31-42							
PARKO STRYP	MODIFICATION METHYLASE BANIII	BACILLUS ANEURINOLYTICUS	184-211							
PARKO STRYP	MODIFICATION METHYLASE BANII	BACILLUS ANEURINOLYTICUS	321-409							
PARKO STRYP	MODIFICATION METHYLASE BSUBI	BACILLUS SUBTILIS	121-148	487-496						
PARKO STRYP	MODIFICATION METHYLASE BSDFI	BACILLUS SUBTILIS	204-231							
PARKO STRYP	MODIFICATION METHYLASE CBFI	CITROBACTER FREUNDII	2-26	312-279						
PARKO STRYP	MODIFICATION METHYLASE HCICI	HENPETOSSIPHON AURANTIACUS	120-147							
PARKO STRYP	MODIFICATION METHYLASE HGCI	HENPETOSSIPHON AURANTIACUS	281-311							
PARKO STRYP	MODIFICATION METHYLASE ECOLI	ESCHERICHIA COLI	76-110	141-172						
PARKO STRYP	MODIFICATION METHYLASE HGBI	HENPETOSSIPHON AURANTIACUS	281-308							
PARKO STRYP	MODIFICATION METHYLASE ECONI	ESCHERICHIA COLI	4-41							
PARKO STRYP	MODIFICATION METHYLASE ECO RV	ESCHERICHIA COLI	73-100							
PARKO STRYP	MODIFICATION METHYLASE FOKI	ENTEROBACTER CLOACAE	418-443							
PARKO STRYP	MODIFICATION METHYLASE FODI	FLAVOBACTERIUM ORGANOZOITES	184-211	279-306	358-415	351-444				
PARKO STRYP	MODIFICATION METHYLASE FROI	FUSOBACTERICUM NUCLEATUM	22-49							
PARKO STRYP	MODIFICATION METHYLASE HAECI	HAEMOPHILUS GALLINARUM	135-165							
PARKO STRYP	MODIFICATION METHYLASE HNCI	HAEMOPHILUS INFLUENZAE	181-208	399-426						
PARKO STRYP	MODIFICATION METHYLASE MTZII	METHANOBACTERIUM THERMOAUTOTrophicum	188-215	396-413						
PARKO STRYP	MODIFICATION METHYLASE CPNI	KLEBSIELLA PNEUMONIAE	270-297							
PARKO STRYP	MODIFICATION METHYLASE DSDVIOBOEPHASE	STREPTOCOCCUS MUTANS	39-46	324-231	349-376					
PARKO STRYP	MODIFICATION METHYLASE MSP1	MORAXELLA SP	5-39	49-104						
PARKO STRYP	MODIFICATION METHYLASE NLAI	NEISSERIA LACTAMICA	124-158	183-210						
PARKO STRYP	MODIFICATION METHYLASE PVU II	PROTEUS VULGARIS	208-235							
PARKO STRYP	MEMBRANE ASSOCIATED ATPESE	SULFOLOBUS ACIDICALDARIUS	9-47							
PARKO STRYP	MODIFICATION METHYLASE PSTI	PROVIDENCIA STUARTII	226-264							
PARKO STRYP	TATYTOPHAN-SPECIFIC TRANSPORT PROTEIN	ESCHERICHIA COLI	10-107							
PARKO STRYP	MODIFICATION METHYLASE STSI	STREPTOCOCCUS SANGUIS	118-153	424-461	600-643					
PARKO STRYP	MODIFICATION METHYLASE SSOI	SHIGELLA SONNEI	81-108							
PARKO STRYP	MODIFICATION METHYLASE SAUPRI	STAPHYLOCOCCUS AUREUS	231-274							
PARKO STRYP	MODIFICATION METHYLASE SCFIIA	LACTOCOCCUS LACTIS	84-113	187-214						
PARKO STRYP	MODIFICATION METHYLASE SCUF-I	LACTOCOCCUS LACTIS	27-41							
PARKO STRYP	MODIFICATION METHYLASE SCUF-II	LACTOCOCCUS LACTIS	188-230	236-290						
PARKO STRYP	CPO DNA METHYLASE	SPHILOPLASMA SP	188-230							
PARKO STRYP	MODIFICATION METHYLASE SWAI	SEARATIA MARCESCENS	61-81							

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PCURSE	1071178-4	Proteolytic Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	ARE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ELK NADIE	PROTEIN	NEISSERIA GONORRHOEA	71-103																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							

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PCGENE	1071170-4	Protein Data Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA
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PCGENE	10/11/10	Prokaryotic Equivalent	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA
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PCGENE	10/11/2004	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462
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PCGENE	10/11/1984	Embryonic Antigens	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	ORGANISM							
REP NAME	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS							
REP1 ECOLI	REPLICATION PROTEIN REPA	ESCHERICHIA COLI	3-16	81-108					
REP2 ECOLI	REPX PROTEIN	BACILLUS SUBTILIS	50-77	90-117					
REP3 ECOLI	REPA PROTEIN	ESCHERICHIA COLI	342-373						
REP4 ECOLI	REPA PROTEIN	ESCHERICHIA COLI	37-84	138-172					
REP5 ECOLI	REPLICATION PROTEIN	NEISSERIA GONORRHOICAE	184-211						
REP6 ECOLI	REPLICATION PROTEIN REPO	LACTOBACILLUS PLANTARUM	234-284						
REP7 ECOLI	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	238-285						
REP8 ECOLI	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	430-467						
REP9 ECOLI	REPA PROTEIN	STREPTOCOCCUS ADALACTIAE	421-467						
REP10 ECOLI	REPX PROTEIN	STREPTOCOCCUS PYOGENES	111-130	173-210					
REP11 ECOLI	REP PROTEIN	STAPHYLOCOCCUS AUREUS	288-315						
REP12 ECOLI	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	108-193	297-334	343-375				
REP13 ECOLI	REPLICATION PROTEIN	CLOSTRIDIUM PERFRINGENS	118-148	203-263					
REP14 ECOLI	REP HELICASE	ESCHERICHIA COLI	119-199	260-317					
REP15 ECOLI	REP PROTEIN	LACTOBACILLUS PLANTARUM	68-102	131-185					
REP16 ECOLI	RESOLVASE	CLOSTRIDIUM PERFRINGENS	34-48						
REP17 ECOLI	PROBABLE PEPTIDE CHAIN RELEASE FACTOR 2	BACILLUS SUBTILIS	86-113	163-204					
REP18 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	86-113	183-204					
REP19 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	SALMONELLA TYPHIMURIUM	180-210	443-473					
REP20 ECOLI	PEPTIDE CHAIN RELEASE FACTOR 3	ESCHERICHIA COLI	199-226						
REP21 ECOLI	1,4-GALACTOSYLTRANSFERASE	ESCHERICHIA COLI	185-212						
REP22 ECOLI	BIOSYNTHESIS PROTEIN RFAO	ESCHERICHIA COLI	39-66	233-268					
REP23 ECOLI	1,2-GLUCOSYLTRANSFERASE	ESCHERICHIA COLI	68-95	145-172	238-263				
REP24 ECOLI	1,2-GLUCOSYLTRANSFERASE	SALMONELLA TYPHIMURIUM	335-369						
REP25 ECOLI	1,2-ACETYLGLUCOSAMINOTRANSFERASE	SALMONELLA TYPHIMURIUM	164-193						
REP26 ECOLI	PEPAK SALTY	ESCHERICHIA COLI	126-160						
REP27 ECOLI	O-ANTIGEN LIASE	SALMONELLA TYPHIMURIUM	8-35	184-240					
REP28 ECOLI	BIOSYNTHESIS PROTEIN RFAF	ESCHERICHIA COLI	63-89						
REP29 ECOLI	BIOSYNTHESIS PROTEIN RFAF	ESCHERICHIA COLI	18-45						
REP30 ECOLI	BIOSYNTHESIS PROTEIN RFAF	ESCHERICHIA COLI	5-30	85-112					
REP31 ECOLI	BIOSYNTHESIS PROTEIN RFAZ	ESCHERICHIA COLI	320-359						
REP32 ECOLI	DTDP-GLUCOSE 4,4-DEHYDRATASE	SALMONELLA TYPHIMURIUM	313-361						
REP33 ECOLI	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE	SALMONELLA TYPHIMURIUM	22-58	205-232					
REP34 ECOLI	PARATOPH SYNTHASE	SALMONELLA TYPHIMURIUM	349-376						
REP35 ECOLI	PRECUSOR FOR YEALIC ANGIUBACTIN	VIBRIO ANGIUBACTIN	81-110						
REP36 ECOLI	PEPTIDE CHAIN RELEASE FACTOR HOMOLOG	ESCHERICHIA COLI	11-48	190-262	310-383				
REP37 ECOLI	PUTATIVE GIB SITE-SPECIFIC RECOMBINASE	BACILLUS THURINGIENSIS	175-202						
REP38 ECOLI	RHAMPOLINOLINASE	ESCHERICHIA COLI	175-202						
REP39 ECOLI	RHAMPOLINOLINASE	SALMONELLA TYPHIMURIUM	106-41						
REP40 ECOLI	L-RHAMNOSYL OXIDON TRANSACTIVATOR	ESCHERICHIA COLI	152-179						
REP41 ECOLI	L-RHAMNOSYL OXIDON REO PROTEIN RHAS	ESCHERICHIA COLI	204-233						
REP42 ECOLI	RHIR REGULATORY PROTEIN	RHIZOBIUM LEGUMINOSARUM	178-185						
REP43 ECOLI	RNA HELICASE RHLBANDRA	ESCHERICHIA COLI	215-242	327-369					
REP44 ECOLI	TRANS TEAM FACTOR RHO	BORRELIA BURGDORFERI	12-109						
REP45 ECOLI	PROTEASE PROD LEO PROTEIN LPA	BACILLUS SUBTILIS	667-694						
REP46 ECOLI	RHSA PROTEIN PRECURSOR	ESCHERICHIA COLI	667-694						
REP47 ECOLI	RHSS PROTEIN PRECURSOR	ESCHERICHIA COLI	670-712						

[illegible]

GENE	INITIALS	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PAN1 ECOLI	RIBONUCLEASE III	ESCHERICHIA COLI	413-440	628-662							
PAN2 ECOLI	RIBONUCLEASE E	ESCHERICHIA COLI	85-114								
PAN3 ECOLI	RIBONUCLEASE P PROTEIN COMPONENT	BUCHNERA APHIDICOLA	159-166								
PAN4 ECOLI	RIBONUCLEASE PH	BACILLUS SUBTILIS	116-160								
PAN5 ECOLI	REGULATORY PROTEIN RNS	ESCHERICHIA COLI	82-109								
PAN6 ECOLI	RIBONUCLEASE	BACILLUS CIRCULANS	38-72								
PAN7 ECOLI	RIBONUCLEASE PRECURSOR	BACILLUS INTERMEDIUS	71-107								
PAN8 ECOLI	RNA POLYMERASE SIGMA-33 FACTOR	BACILLUS THURINGIENSIS	10-37								
PAN9 ECOLI	RNA POLYMERASE SIGMA-33 FACTOR	CITROBACTER FREUNDII	9-35	61-90							
PAN10 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	ALCALIGENES EUTROPHUS	229-266								
PAN11 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	AZONHIZOBIVUM CAULODANS	174-201								
PAN12 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	BACILLUS SUBTILIS	18-43	97-124	274-308	394-423					
PAN13 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	BRADYRHIZOBIVUM JAPONICUM	97-124								
PAN14 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	KLEBSIELLA PNEUMONIAE	148-182								
PAN15 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	RHODOSPIRILLUM RUBRUM	155-185								
PAN16 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	BRADYRHIZOBIVUM JAPONICUM	148-182								
PAN17 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	ALCALIGENES EUTROPHUS	229-266								
PAN18 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	ESCHERICHIA COLI	21-47								
PAN19 ECOLI	RNA POLYMERASE SIGMA-54 FACTOR	SALMONELLA TYPHIMURUM	31-47								
PAN20 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	BUCHNERA APHIDICOLA	69-96	109-136	173-217	228-255	301-337				
PAN21 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	CHLAMYDOMONAS RABIDULATIS	3-33								
PAN22 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	327-361								
PAN23 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	PSUDOMONAS AERUGINOSA	374-388								
PAN24 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	RICKETTSIA PROWAZEKII	244-251	248-282							
PAN25 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYXOCOCCUS XANTHUS	208-235	118-147	335-366						
PAN26 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	STREPTOCOCCUS SP	185-207								
PAN27 ECOLI	BILIN BIOSYNTHESIS PROTEIN NCP	BACILLUS SUBTILIS	31-107								
PAN28 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	31-107								
PAN29 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	SALMONELLA TYPHIMURUM	31-107								
PAN30 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	HALOBACTERIUM HALOBIVUM	661-904								
PAN31 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	HALOCOCCLUS MONILIVUS	315-370								
PAN32 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	METHANOBACTERIUM THERMAUTOTROPHICUM	211-241	416-517	647-669						
PAN33 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	SULFOLOBUS ACIDOCALDARIUS	222-256	500-537	697-730						
PAN34 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	THEMOCOCCLUS CELER	228-262								
PAN35 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	399-428	101-103							
PAN36 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	108-111							
PAN37 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	SALMONELLA TYPHIMURUM	399-428	101-103							
PAN38 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	SULFOLOBUS ACIDOCALDARIUS	160-187	531-561	937-961						
PAN39 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	THEMOCOCCLUS CELER	399-428	101-103							
PAN40 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ANABENA SP	152-194								
PAN41 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	ESCHERICHIA COLI	399-428	101-103							
PAN42 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	HALOBACTERIUM HALOBIVUM	175-202								
PAN43 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	HALOCOCCLUS MONILIVUS	37-34	117-144	207-234						
PAN44 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	METHANOBACTERIUM THERMAUTOTROPHICUM	38-45	372-392	337-374						
PAN45 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN46 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN47 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN48 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN49 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN50 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN51 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN52 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN53 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN54 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN55 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN56 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN57 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN58 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN59 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN60 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN61 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN62 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN63 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN64 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN65 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN66 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN67 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN68 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN69 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN70 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN71 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN72 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN73 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN74 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN75 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN76 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN77 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN78 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN79 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN80 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN81 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN82 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN83 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN84 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN85 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN86 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN87 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN88 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN89 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN90 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN91 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN92 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN93 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN94 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN95 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN96 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN97 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN98 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN99 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					
PAN100 ECOLI	RNA POLYMERASE SIGMA-70 FACTOR	MYCOBACTERIUM LEPTAE	323-360	600-617	911-938	1131-1158					

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PCGENE	1071171.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462
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[illegible]

FCCLN	IDENTIFIER	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ILLNAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PT11	ECOLI	LYSYL-TRNA SYNTHETASE	289-310	289-310							
PT12	ECOLI	LYSYL-TRNA SYNTHETASE, HEAT INDUCIBLE	45-72	289-310							
PT13	ECOLI	LEUCYL-TRNA SYNTHETASE	335-347								
PT14	ECOLI	LEUCYL-TRNA SYNTHETASE	66-99								
PT15	BACST	METHIONYL-TRNA SYNTHETASE	81-124								
PT16	ECOLI	METHIONYL-TRNA SYNTHETASE	341-348								
PT17	ECOLI	PROLYL-TRNA SYNTHETASE	349-421								
PT18	ECOLI	GLUTAMINYL-TRNA SYNTHETASE	449-483								
PT19	PSEV	STAD PROTEIN	340-374								
PT20	ECOLI	ARGINYL-TRNA SYNTHETASE	401-428	409-419							
PT21	BACST	THREONYL-TRNA SYNTHETASE	601-610	609-643							
PT22	BACST	VALYL-TRNA SYNTHETASE	1009-1027	1013-912	924-931						
PT23	ECOLI	VALYL-TRNA SYNTHETASE	204-231	219-246							
PT24	BACST	THYROSINYL-TRNA SYNTHETASE	81-115	375-409							
PT25	BACST	THYROSYL-TRNA SYNTHETASE 1	10-96								
PT26	BACST	THYROSYL-TRNA SYNTHETASE 2	291-323	372-416							
PT27	BACST	THYROSYL-TRNA SYNTHETASE	195-222	372-416							
PT28	ECOLI	ENZYME ECOL1200 LN PROTEIN	126-167	405-432	483-512						
PT29	ECOLI	ENZYME ECOL1200 R PROTEIN	10-37	624-431	702-726	768-795	847-870	964-1000			
PT30	ECOLI	ENZYME ECOL1 R PROTEIN	18-263								
PT31	ECOLI	ENZYME ECOL1200 I SPECIFICITY PROTEIN	114-181								
PT32	ECOLI	ENZYME ECOL1 SPECIFICITY PROTEIN	279-306								
PT33	ECOLI	ENZYME ECOL1 SPECIFICITY PROTEIN	279-312								
PT34	ECOLI	ENZYME ECOL1 SPECIFICITY PROTEIN	249-283								
PT35	ECOLI	ENZYME ECOL1 SPECIFICITY PROTEIN	279-306								
PT36	SALPO	ENZYME SPECIFICITY PROTEIN	198-423								
PT37	SALTY	ENZYME SPECIFICITY PROTEIN	194-221	276-304	403-429						
PT38	ECOLI	ENZYME SPECIFICITY PROTEIN	138-196	283-293	408-440	619-682	687-728	924-954			
PT39	ACET	ACETONACTER CALCOACEICUS	46-76								
PT40	ECOLI	TYPE II RESTRICTION ENZYME ACCI	1-43	135-233	374-380						
PT41	BACST	TYPE II RESTRICTION ENZYME BSUR1	1-43	338-384	401-430	532-559					
PT42	ECOLI	TYPE II RESTRICTION ENZYME BSUR2	33-62								
PT43	CITR	CITROBACTER FREUNDII	176-315								
PT44	HERP	HERPETOSEPHON ALUMINATIGUS	201-273								
PT45	HERP	HERPETOSEPHON ALUMINATIGUS	181-223								
PT46	DESUL	DESULFOVIBRIO DESULFOFUCANS	213-240								
PT47	STREPT	STREPTOCOCCUS PNEUMONIAE	2-29								
PT48	ECOLI	ESCHERICHIA COLI	331-360								
PT49	ECOLI	ESCHERICHIA COLI	138-155	214-241							
PT50	FLA	FLAVOBACTERIUM OKENOKOITES	302-336								
PT51	FLAOK	FLAVOBACTERIUM OKENOKOITES	6-38	69-96							
PT52	HAEM	HAEMOPHILUS INFLUENZAE	77-123								
PT53	HAEM	HAEMOPHILUS INFLUENZAE	21-50								
PT54	HAEM	HAEMOPHILUS INFLUENZAE	91-138								
PT55	HAEM	HAEMOPHILUS INFLUENZAE	18-43	174-205							
PT56	MOXA	MORAXELLA BOVIS	15-41	182-213	223-232						
PT57	MOXA	MORAXELLA BOVIS	3-30	158-183	317-364						
PT58	MORBO	MORAXELLA BOVIS	104-153								
PT59	METH	METHANOBACTERIUM THERMOFORMICULUM	117-144	231-258							
PT60	NEIG	NEISSERIA GONORRHOEAE	5-32	41-48	395-446						
PT61	STREPT	STREPTOCOCCUS SANGUIS	206-263	318-318							
PT62	SHIG	SHIGELLA SONNEI	70-102								
PT63	STAPH	STAPHYLOCOCCUS AUREUS	144-181								
PT64	SALMON	SALMONELLA INFANTIS	61-88								
PT65	SERR	SERRATIA MARCESCENS	147-181	202-237							
PT66	THER	THERMOAQUATICUS	27-31	75-102	216-286	371-403					
PT67	ECOLI	ESCHERICHIA COLI	62-89	254-313							
PT68	BACST	SYSTEM ENZYME RES									

[illegible]

PCGENE	10211314	Protein/peptide Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
ORGANISM	BACILLUS	BACILLUS THERMOPROTEOLYTICUS	86-113						
PTHER BACTH	THERMOLYSIN	THERMOLYSIN	131-141						
PTHER THERV	THERMITASE	THERMITASE	325-361	301-328					
PTHIC ECOLI	THIC PROTEIN	ESCHERICHIA COLI	128-145						
PTHIO ECOLI	THIO PROTEIN	ESCHERICHIA COLI	128-145	199-333					
PTIPS SULAC	THIAMOPIN PRECURSOR	SULFOLOBUS ACIDICUS-ALDARIUS	288-315						
PTIRONE SYNTHASE	THIRONE SYNTHASE	BREVIBACTERIUM LACTOFERMENTUM	69-96						
PTIRAC SACER	PUTATIVE THIOL SULFATE SULTUR TRANSFERASE	SACCHAROPOLYSPORA ERYTHRAEA	144-171						
PTIC ECOLI	THIOGROW FACTOR	ESCHERICHIA COLI	216-266						
PTIPA TREPA	TREPONEMAL MEMBRANE PROTEIN A PRECURSOR	TREPONEMA PALLIDUM	44-71						
PTIPB TREPA	TREPONEMAL MEMBRANE PROTEIN B PRECURSOR	TREPONEMA PALLIDUM	41-68						
PTIPB TREPH	TREPONEMAL MEMBRANE PROTEIN C PRECURSOR	TREPONEMA PHAGEDENIS	74-108						
PTINAB ECOLI	LOW AFFINITY TRYPTOPHAN PERMEASE	ESCHERICHIA COLI	32-79	322-349					
PTNPA STAAU	TRANSPOSASE A	STAPHYLOCOCCUS AUREUS	39-97	111-138					
PTNPA STAAU	TRANSPOSASE B	STAPHYLOCOCCUS AUREUS	151-178						
PTNPI BACTO	TNP I RESOLVASE	BACILLUS THURINGIENSIS	189-235		174-201				
PTNPI ECOLI	TRANSPOSIN TNP1	ESCHERICHIA COLI	743	65-93	310-337				
PTNPI ECOLI	TRANSPOSIN TNP2	ESCHERICHIA COLI	32-59	314-341					
PTNPI ECOLI	TRANSPOSIN TNP3	ESCHERICHIA COLI	339-366						
PTNPI ECOLI	TRANSPOSIN TNP4	ESCHERICHIA COLI	461-490						
PTNPI ECOLI	TRANSPOSIN TNP5	ESCHERICHIA COLI	76-83						
PTNPI ECOLI	TRANSPOSIN TNP6	ESCHERICHIA COLI	119-133						
PTNPI ECOLI	TRANSPOSIN TNP7	ESCHERICHIA COLI	179-213						
PTNPI ECOLI	TRANSPOSIN TNP8	ESCHERICHIA COLI	143-170						
PTNPI ECOLI	TRANSPOSIN TNP9	ESCHERICHIA COLI	101-138						
PTNPI ECOLI	TRANSPOSIN TNP10	ESCHERICHIA COLI	143-178	184-211	219-266	318-343			
PTNPI ECOLI	TRANSPOSIN TNP11	ESCHERICHIA COLI	203-230						
PTNPI ECOLI	TRANSPOSIN TNP12	ESCHERICHIA COLI	797-824						
PTNPI ECOLI	TRANSPOSIN TNP13	ESCHERICHIA COLI	179-206						
PTNPI ECOLI	TRANSPOSIN TNP14	ESCHERICHIA COLI	54-83						
PTNPI ECOLI	TRANSPOSIN TNP15	ESCHERICHIA COLI	20-88	99-139	204-231	332-414	847-963	966-994	1348-1402
PTNPI ECOLI	TRANSPOSIN TNP16	ESCHERICHIA COLI	470-497						
PTNPI ECOLI	TRANSPOSIN TNP17	ESCHERICHIA COLI	13-40	133-163	199-241	835-869	923-950	1334-1388	1403-1433
PTNPI ECOLI	TRANSPOSIN TNP18	ESCHERICHIA COLI	106-143						
PTNPI ECOLI	TRANSPOSIN TNP19	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP20	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP21	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP22	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP23	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP24	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP25	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP26	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP27	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP28	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP29	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP30	ESCHERICHIA COLI	13-40						
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PTNPI ECOLI	TRANSPOSIN TNP35	ESCHERICHIA COLI	13-40						
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PTNPI ECOLI	TRANSPOSIN TNP39	ESCHERICHIA COLI	13-40						
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PTNPI ECOLI	TRANSPOSIN TNP145	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP146	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP147	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP148	ESCHERICHIA COLI	13-40						
PTNPI ECOLI	TRANSPOSIN TNP149	ESCHERICHIA COLI	1						

[illegible]

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PCGENE	10/21/19-4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AR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ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

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Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AR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TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

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PCGENE	101317842 Multi Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE NAME	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
P411 HUMAN	NON-ERYTHROID PROTEIN 4.1 (BAND 4.1, LYMPHOID FORM)	170-215	170-215							
P42 HUMAN	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2	173-209	173-209	518-543						
P47 HUMAN	CD3 CELL-SURFACE ANTIGEN HEAVY CHAIN (P31HC) (LYMPHOCYTE ACTIVATION)	281-325	281-325							
PHIE HUMAN	5-HYDROXYTRYPTAMINE 1F RECEPTOR (5-HT-1F) (SEROTONIN RECEPTOR)	311-338	311-338							
PHIF HUMAN	5-HYDROXYTRYPTAMINE 1F RECEPTOR (5-HT-1F) (SEROTONIN RECEPTOR)	322-353	322-353							
PHIA HUMAN	5-HYDROXYTRYPTAMINE 2A RECEPTOR (5-HT-2A) (SEROTONIN RECEPTOR)	32-56	32-56							
PHIT HUMAN	5-HYDROXYTRYPTAMINE 2 RECEPTOR (5-HT-2) (5-HT-2) (SEROTONIN RECEPTOR)	72-99	72-99	330-357						
PALAC HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ACT)	98-122	98-122							
PALAO HUMAN	ALPHA-1-ACID GLYCOPROTEIN 1 PRECURSOR (OROSOMUCOID) (OROI)	92-119	92-119							
PALAT HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) PROTEASE INHIBITOR (ALPHA-1)	148-202	148-202							
PALAU HUMAN	ALPHA-1-ANTITRYPSIN-RELATED PROTEIN PRECURSOR	183-197	183-197							
PAPAP HUMAN	ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) PLASMIN INHIBITOR (ALPHA-1)	191-218	191-218	365-395						
PASOL HUMAN	LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	104-134	104-134							
PASAO HUMAN	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2M)	51-80	51-80	319-349	1051-1112	1402-1426				
PAT HUMAN	ALZHEIMER'S DISEASE AMYLOID A1 PROTEIN PRECURSOR (PROTEASE NEKIN-II)	237-455	237-455							
PACTT HUMAN	ALPHA-ACTONIN (P-ACTIN CROSS LINKING PROTEIN)	92-119	92-119	720-747						
PACTM HUMAN	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.1)	106-136	106-136							
PAPTA HUMAN	ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMUSCLE FILAXIN)	61-88	61-88	119-147	3604-7633					
PACTS HUMAN	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1)	305-333	305-333							
PACTI HUMAN	ACTIVATOR 1 740 KD SUBUNIT (REPLICATION FACTOR C 740 KD SUBUNIT) (A1)	14-51	182-209	641-700						
PACOL HUMAN	ACTYL-COA DEHYDROGENASE PRECURSOR, LONG-CHAIN SPECIFIC (EC 1.3.9.13)	78-108	179-206	313-340						
PACTC HUMAN	ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, TESTIS-SPECIFIC (EC 3.4.13.1)	76-113	126-153	616-710						
PACTE HUMAN	ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, SOMATIC (EC 3.4.13.1) (ACE)	632-689	700-727	1250-1284						
PACHA HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA CHAIN PRECURSOR	48-90								
PACHE HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, EPSILON CHAIN PRECURSOR	48-90								
PACHO HUMAN	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	61-79	304-331							
PACHP HUMAN	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-4 CHAIN (P-RAGNIENT)	35-56	70-97							
PACHS HUMAN	ACERIN PRECURSOR (EC 3.4.21.10)	122-149								
PACTA HUMAN	ACT PHOSPHATASE, MUSCLE TYPE ISOZYME (EC 3.1.3.7) (ACT PHOSPHATE)	36-51								
PACTI HUMAN	ADP-ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)	162-189								
PACTS HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM 1 (ADP/ATP TRANSLOCASE 3)	163-190								
PACTS HUMAN	ADP-ATP CARRIER PROTEIN 19 (ADP/ATP TRANSLOCASE 3)	197-238	381-414							
PALFA HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (MUSCLE)	34-43								
PALFB HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (LIVER)	78-113								
PALFD HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFE HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFH HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFI HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
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PALFK HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
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PALFM HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFN HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFO HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
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PALFX HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFY HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFZ HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFA HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFB HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFC HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFD HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFE HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFH HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFI HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR (ALPHA-1) (DEVELOPMENTAL)	99-106								
PALFJ HUMAN	ALFA-1-ANTITRYPSIN PRECURSOR									

[illegible]

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PCGENE	1071116d Mail Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PERC1 HUMAN	EXCISION REPAIR PROTEIN ERCC-4	146-309						
PERC2 HUMAN	EXTENSION RECEPTOR (ER)	431-488						
PERC3 HUMAN	ENDOTHELIN-1 PRECURSOR (ET-1)	131-160						
PERC4 HUMAN	ENDOTHELIN-2 PRECURSOR (ET-2)	182-309						
PERC5 HUMAN	EVEXA PROTEIN PRECURSOR	29-36						
PERC6 HUMAN	EXAM (PIL) (GYTOVILLIN) (VILIN-3)	116-144	331-393	403-439	312-539			
PERC7 HUMAN	COAGULATION FACTOR V PRECURSOR	2100-2127						
PERC8 HUMAN	COAGULATION FACTOR VIII PRECURSOR (PROCOAGULANT COMPONENT)	371-900	1007-1034	1194-1230				
PERC9 HUMAN	COAGULATION FACTOR IX PRECURSOR (EC 3.2.3.32) (CROTININ FACTOR)	371-398						
PERC10 HUMAN	FATTY ACID-BINDING PROTEIN, INTESTINAL	96-125						
PERC11 HUMAN	APOTOSIS-MEDIATING SURFACE ANTIGEN FAS PRECURSOR (APO-1 ANTIGEN)	33-50	249-301	306-333				
PERC12 HUMAN	LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (L YMOHOCYTE IGE	31-113						
PERC13 HUMAN	HIGH AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (L YMOHOCYTE IGE	140-174						
PERC14 HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR (EC 2.1.1.12)	110-337						
PERC15 HUMAN	FIBRINOGEN ALPHA CHAIN PRECURSOR	131-163	421-453					
PERC16 HUMAN	FIBRINOGEN BETA CHAIN PRECURSOR	149-184						
PERC17 HUMAN	FIBRINOGEN GAMMA-A CHAIN PRECURSOR	59-93	123-160					
PERC18 HUMAN	FIBRINOGEN GAMMA-B CHAIN (FIBRINOGEN GAMMA)	59-93	123-160					
PERC19 HUMAN	FIBRINECTIN PRECURSOR	2168-2199						
PERC20 HUMAN	FLI-1 ONCOGENE (ELONG TRANSCRIPTION FACTOR)	172-209						
PERC21 HUMAN	5-DEHYDROXYLANTHINE MONOOXYGENASE (N-OXIDE FORMING) 3 (EC 1.1.1.3.8)	184-218	336-383	301-328				
PERC22 HUMAN	P53-C FOR PROTO-ONCOGENE PROTEIN	162-193						
PERC23 HUMAN	FG3-RELATED ANTIGEN 1	133-168						
PERC24 HUMAN	FG3-RELATED ANTIGEN 2	146-180						
PERC25 HUMAN	FEARITIN HEAVY CHAIN	3-24						
PERC26 HUMAN	FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R)	3-23						
PERC27 HUMAN	TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 3.2.1.11) (ALPHA-L-FUCOSIDASE	384-393						
PERC28 HUMAN	FUMARATE HYDRATASE, MITOCHONDRIAL (EC 4.2.1.3) (FUMALASE)	308-333						
PERC29 HUMAN	MUTATIVE LYMPHOCYTE G0/G1 SWITCH PROTEIN	424-451						
PERC30 HUMAN	PROTEIN KINASE C SUBSTRATE, 40 KD PROTEIN HEAVY CHAIN (PKC-H)	56-83						
PERC31 HUMAN	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (PHOSPHOGLUCOSE	146-173						
PERC32 HUMAN	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GAT31.2 PRECURSOR	18-30						
PERC33 HUMAN	GALACTOGENASE 3 (EC 3.1.1.6)	181-215						
PERC34 HUMAN	GALACTOGENASE 3 (EC 3.1.1.6)	334-381						
PERC35 HUMAN	GALMA-AMINO BUTYRIC ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA1A)	210-237						
PERC36 HUMAN	GALMA-AMINO BUTYRIC ACID RECEPTOR ALPHA-2 SUBUNIT PRECURSOR (GABA2A)	210-237						
PERC37 HUMAN	GASTROCHELYTOKININ TYPE B RECEPTOR (CCR-9 RECEPTOR)	311-335						
PERC38 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 1	73-103						
PERC39 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 2	33-49						
PERC40 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 3	33-49						
PERC41 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 4	33-49						
PERC42 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 5	33-49						
PERC43 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 6	33-49						
PERC44 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 7	33-49						
PERC45 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 8	33-49						
PERC46 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 9	33-49						
PERC47 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 10	33-49						
PERC48 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 11	33-49						
PERC49 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 12	33-49						
PERC50 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 13	33-49						
PERC51 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 14	33-49						
PERC52 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 15	33-49						
PERC53 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 16	33-49						
PERC54 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 17	33-49						
PERC55 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 18	33-49						
PERC56 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 19	33-49						
PERC57 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 20	33-49						
PERC58 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 21	33-49						
PERC59 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 22	33-49						
PERC60 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 23	33-49						
PERC61 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 24	33-49						
PERC62 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 25	33-49						
PERC63 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 26	33-49						
PERC64 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 27	33-49						
PERC65 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 28	33-49						
PERC66 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 29	33-49						
PERC67 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 30	33-49						
PERC68 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 31	33-49						
PERC69 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 32	33-49						
PERC70 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 33	33-49						
PERC71 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 34	33-49						
PERC72 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 35	33-49						
PERC73 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 36	33-49						
PERC74 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 37	33-49						
PERC75 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 38	33-49						
PERC76 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 39	33-49						
PERC77 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 40	33-49						
PERC78 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 41	33-49						
PERC79 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 42	33-49						
PERC80 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 43	33-49						
PERC81 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 44	33-49						
PERC82 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 45	33-49						
PERC83 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 46	33-49						
PERC84 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 47	33-49						
PERC85 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 48	33-49						
PERC86 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 49	33-49						
PERC87 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 50	33-49						
PERC88 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 51	33-49						
PERC89 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 52	33-49						
PERC90 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 53	33-49						
PERC91 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 54	33-49						
PERC92 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 55	33-49						
PERC93 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 56	33-49						
PERC94 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 57	33-49						
PERC95 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 58	33-49						
PERC96 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 59	33-49						
PERC97 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 60	33-49						
PERC98 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 61	33-49						
PERC99 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 62	33-49						
PERC100 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 63	33-49						
PERC101 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 64	33-49						
PERC102 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 65	33-49						
PERC103 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 66	33-49						
PERC104 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 67	33-49						
PERC105 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 68	33-49						
PERC106 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 69	33-49						
PERC107 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 70	33-49						
PERC108 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 71	33-49						
PERC109 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 72	33-49						
PERC110 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 73	33-49						
PERC111 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 74	33-49						
PERC112 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 75	33-49						
PERC113 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 76	33-49						
PERC114 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 77	33-49						
PERC115 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 78	33-49						
PERC116 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 79	33-49						
PERC117 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 80	33-49						
PERC118 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 81	33-49						
PERC119 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 82	33-49						
PERC120 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 83	33-49						
PERC121 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 84	33-49						
PERC122 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 85	33-49						
PERC123 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 86	33-49						
PERC124 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 87	33-49						
PERC125 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 88	33-49						
PERC126 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 89	33-49						
PERC127 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 90	33-49						
PERC128 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 91	33-49						
PERC129 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 92	33-49						
PERC130 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 93	33-49						
PERC131 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 94	33-49						
PERC132 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 95	33-49						
PERC133 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 96	33-49						
PERC134 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 97	33-49						
PERC135 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 98	33-49						
PERC136 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 99	33-49						
PERC137 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 100	33-49						
PERC138 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 101	33-49						
PERC139 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 102	33-49						
PERC140 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 103	33-49						
PERC141 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 104	33-49						
PERC142 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 105	33-49						
PERC143 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 106	33-49						
PERC144 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 107	33-49						
PERC145 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 108	33-49						
PERC146 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 109	33-49						
PERC147 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 110	33-49						
PERC148 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 111	33-49						
PERC149 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 112	33-49						
PERC150 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 113	33-49						
PERC151 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 114	33-49						
PERC152 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 115	33-49						
PERC153 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 116	33-49						
PERC154 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 117	33-49						
PERC155 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 118	33-49						
PERC156 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 119	33-49						
PERC157 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN GQI, ALPHA SUBUNIT 120	33-49</						

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FILE NAME	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
POLY2 HUMAN	SEADNE HYDROXYMETHYL TRANSFERASE, MITOCHONDRIAL (EC 2.1.2.1) (SEADNE)	471-484							
POLY3 HUMAN	14 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN)	584-591							
POLY4 HUMAN	GLYCINE RECEPTOR ALPHA-3 CHAIN PRECURSOR	142-169							
POLY5 HUMAN	GLA VIN (FRAGMENT)	9-43							
POLY6 HUMAN	GROWTH HORMONE-RELEASING HORMONE RECEPTOR PRECURSOR (GHRH RECEPTOR)	13-153							
POLY7 HUMAN	GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3.1.19) (GTHS) (CLASS)	64-91							
POLY8 HUMAN	GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3.1.19) (GTHS) (CLASS)	474-581							
POLY9 HUMAN	GLUTATHIONE S-TRANSFERASE HA SUBUNIT 2 (EC 2.3.1.19) (GTHS) (CLASS)	274-301							
POLY10 HUMAN	GLUCOSE TRANSPORTER TYPE 1, ENTEROCYTE/BILAIN	272-299							
POLY11 HUMAN	GLUCOSE TRANSPORTER TYPE 1, BRAIN	290-317							
POLY12 HUMAN	GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE	44-89							
PHI1 HUMAN	HISTONE H1	73-104							
PHI2 HUMAN	HISTONE H1A (H1.1)	70-101							
PHI3 HUMAN	HISTONE H1B (H1.4)	71-102							
PHI4 HUMAN	HISTONE H1C (H1.5)	70-101							
PHI5 HUMAN	HISTONE H1D (H1.2)	74-103							
PHI6 HUMAN	HISTONE H1E	30-47							
PHI7 HUMAN	HISTONE H2B.1	30-47							
PHI8 HUMAN	HISTONE H2B.2	30-47							
PHI9 HUMAN	HISTONE H2B (H2B.1 A)	30-47							
PHI10 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	142-169							
PHI11 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	36-83							
PHI12 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	30-37							
PHI13 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	30-37							
PHI14 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	16-41							
PHI15 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DRB1 (H2B.1 A)	101-129							
PHI16 HUMAN	HEPATIC-BINDING GROWTH FACTOR PRECURSOR 1 (HBGF-1) (ACIDIC FIBROBLAST)	61-91							
PHI17 HUMAN	HBGF-2 PROTO-ONCOGENE PROTEIN PRECURSOR (HBGF-2)	41-73							
PHI18 HUMAN	FIBROBLAST GROWTH FACTOR 3 PRECURSOR (FGF-3) (HBGF-4) (HGF-2)	159-186							
PHI19 HUMAN	PROTEIN (RSP BINDING DOMAINS) (HGF-1) (HGF-2) (HGF-3) (HGF-4) (HGF-5)	342-312							
PHI20 HUMAN	PROTEIN (RSP BINDING DOMAINS) (HGF-1) (HGF-2) (HGF-3) (HGF-4) (HGF-5)	74-118							
PHI21 HUMAN	PROTEIN (RSP BINDING DOMAINS) (HGF-1) (HGF-2) (HGF-3) (HGF-4) (HGF-5)	169-196							
PHI22 HUMAN	PROTEIN (RSP BINDING DOMAINS) (HGF-1) (HGF-2) (HGF-3) (HGF-4) (HGF-5)	27-49							
PHI23 HUMAN	PROTEIN (RSP BINDING DOMAINS) (HGF-1) (HGF-2) (HGF-3) (HGF-4) (HGF-5)	336-353							
PHI24 HUMAN	BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 2.1.1.33) (N-ACETYL-)	188-415							
PHI25 HUMAN	BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 2.1.1.33) (N-ACETYL-)	176-212							
PHI26 HUMAN	HOMEOBOX PROTEIN HESX-1 (HESX-1)	2-39							
PHI27 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	197-234							
PHI28 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	206-333							
PHI29 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	331-548							
PHI30 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	42-76							
PHI31 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	443-476							
PHI32 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	311-543							
PHI33 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	113-140							
PHI34 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	164-209							
PHI35 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	117-194							
PHI36 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	67-108							
PHI37 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	47-74							
PHI38 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	262-289							
PHI39 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	135-162							
PHI40 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	33-40							
PHI41 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	183-210							
PHI42 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	331-378							
PHI43 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	51-44							
PHI44 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	474-504							
PHI45 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	322-349							
PHI46 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	406-413							
PHI47 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	108-149							
PHI48 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	105-107							
PHI49 HUMAN	HEPATOCTYB NUCLEAR FACTOR 1 (HNF-1A) (LIVER SPECIFIC)	172-199							

GENE	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PILK1 HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL-1RI) (P60)	437-487									
PIL13 HUMAN	INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR (IL-1RII)	139-186									
PILK2 HUMAN	INTERLEUKIN-3 RECEPTOR ALPHA CHAIN PRECURSOR (IL-3R-ALPHA)	97-114									
PILK3 HUMAN	INTERLEUKIN-4 RECEPTOR (IL-4) (B-CELL STIMULATORY FACTOR 2) (BSF-2)	112-119									
PILK4 HUMAN	INTERLEUKIN-6 RECEPTOR	94-121									
PILK5 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (IL-6-ALPHA-REC)	90-117	164-191	300-327	308-333						
PILK6 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (FIBROBLAST)	88-129									
PILK7 HUMAN	INTERLEUKIN-6 RECEPTOR (CONTAINS INTERLEUKIN-INDUCED 11 KD)	92-131									
PILK8 HUMAN	INTERLEUKIN-6 RECEPTOR (CONTAINS INTERLEUKIN-INDUCED 17 KD PROTEIN (IL-6-17K))	51-78	216-245	393-420							
PILK9 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	192-419									
PILK10 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	119-148	229-273	326-363	316-410						
PILK11 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-182									
PILK12 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	90-117	206-233								
PILK13 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	137-163									
PILK14 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	235-262	900-927								
PILK15 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	330-314	637-693	763-792							
PILK16 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	824-911	844-974								
PILK17 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	104-107	310-341	793-822							
PILK18 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	104-107									
PILK19 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	330-344									
PILK20 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	314-343	334-369								
PILK21 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	335-366	763-792								
PILK22 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	334-351									
PILK23 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	342-349									
PILK24 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	342-351									
PILK25 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	311-318	333-393								
PILK26 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	353-399	604-637								
PILK27 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	134-161	433-432	772-818							
PILK28 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	154-187	196-237	337-399	478-462						
PILK29 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	113-122	306-335	193-424							
PILK30 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	113-143									
PILK31 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	308-339	302-346	393-431							
PILK32 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	122-132	331-398	337-385							
PILK33 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	17-114	317-363	376-397							
PILK34 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	18-118	317-363	376-397							
PILK35 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	194-210	346-384	390-463							
PILK36 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	215-248	364-405	461-483							
PILK37 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	42-73	126-153	185-248							
PILK38 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	183-248	332-373								
PILK39 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	178-238	333-366	421-449							
PILK40 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	140-167									
PILK41 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	7-34	130-161	217-244							
PILK42 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	140-167									
PILK43 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	49-80	131-159								
PILK44 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	49-80									
PILK45 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	37-43									
PILK46 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	180-414									
PILK47 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	179-206									
PILK48 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK49 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK50 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK51 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK52 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK53 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK54 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK55 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK56 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK57 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK58 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK59 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK60 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK61 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK62 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK63 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK64 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK65 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK66 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK67 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK68 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK69 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK70 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK71 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK72 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK73 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK74 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK75 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK76 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK77 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK78 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK79 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK80 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK81 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK82 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK83 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK84 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK85 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK86 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK87 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK88 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK89 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK90 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK91 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK92 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK93 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK94 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK95 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK96 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK97 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK98 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK99 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									
PILK100 HUMAN	INTERLEUKIN-6 RECEPTOR PRECURSOR (EC 2.1.1.12) (IL-6)	171-204									

PROTEIN	107175ed Manif Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PRF1	HUMAN PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FES/PS (EC 2.1.1.112) (C-FES)	101-145	291-322					
PRF2	HUMAN RECEPTOR-RELATED TYROSINE KINASE FLT PRECURSOR (EC 2.1.1.112)	204-235	319-353					
PRF3	HUMAN MACROPHAGE COLONY STIMULATING FACTOR 1 RECEPTOR PRECURSOR (CSF-1-R)	393-520						
PRF4	HUMAN PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN (EC 2.1.1.112) (P94-FYN)	199-333						
PRF5	HUMAN G2AP DEPENDENT PROTEIN KINASE BETA ISOZYME (G2K) (EC 2.1.1.37)	17-34						
PRF6	HUMAN TYROSINE KINASE DEX RECEPTOR PRECURSOR (EC 2.1.1.112)	848-935						
PRF7	HUMAN KUNLEIN HEAVY CHAIN	126-155	435-452	613-640	645-716	872-899		
PRF8	HUMAN KIT PROTO-ONCOGENE TYROSINE KINASE PRECURSOR (EC 2.1.1.112)	235-267						
PRF9	HUMAN HEPATOCYTE GROWTH FACTOR RECEPTOR (HGF RECEPTOR) (MET) (EC 2.1.1.112)	898-923						
PRF10	HUMAN KINOMENIN RECEPTOR (ALPHA-2-THIO) (PROTEINASE INHIBITOR)	905-932						
PRF11	HUMAN GALLICACIDYLTRANSFERASE ASSOCIATED PROTEIN KINASE PIGITA (EC 2.1.1.1)	81-108						
PRF12	HUMAN INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE	149-176	191-235	315-312				
PRF13	HUMAN PUTATIVE BEAD/THREONINE-PROTEIN KINASE PH (EC 2.1.1.1)	383-409						
PRF14	HUMAN PUTATIVE BEAD/THREONINE-PROTEIN KINASE PH (EC 2.1.1.1) (PKC-4)	318-345						
PRF15	HUMAN SERINE/THREONINE-PROTEIN KINASE PCTAIRE-1 (EC 2.1.1.1)	149-176	209-235					
PRF16	HUMAN PYRUVATE KINASE M1 (MUSCLE) ISOZYME (EC 2.1.1.40) (CYTOSOLIC THYROID)	243-269						
PRF17	HUMAN PYRUVATE KINASE M2 ISOZYME (EC 2.1.1.40)	243-269						
PRF18	HUMAN PYRUVATE KINASE ISOZYME A (EC 2.1.1.40)	3-29						
PRF19	HUMAN PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RET (EC 2.1.1.112)	183-212						
PRF20	HUMAN KOS PROTO-ONCOGENE TYROSINE KINASE (EC 2.1.1.112) (FRAGMENT)	153-200						
PRF21	HUMAN PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.1.1.112) (P86-SRC)	143-170						
PRF22	HUMAN LURIN KU AUTOANTIGEN PROTEIN P10 (70 KD SUBUNIT OF KU ANTIGEN)	235-279						
PRF23	HUMAN LURIN KU AUTOANTIGEN PROTEIN P44 (84 KD SUBUNIT OF KU ANTIGEN)	318-393						
PRF24	HUMAN PROTO-ONCOGENE TYROSINE-PROTEIN KINASE YES (EC 2.1.1.112) (P41-YES)	209-241						
PRF25	HUMAN LAMIN B1	13-46	117-144	155-193	314-341	397-424	480-507	510-539
PRF26	HUMAN LAMIN A (70 KD LAMIN)	33-48	114-165	292-343				
PRF27	HUMAN LAMIN C	33-48	114-165	292-343				
PRF28	HUMAN LAMIN B2	933-949						
PRF29	HUMAN LAMIN B1	191-222	291-343					
PRF30	HUMAN PHOSPHATIDYLCHOLINE STEROID ACYLTRANSFERASE PRECURSOR (EC 2.1.1.43)	131-158						
PRF31	HUMAN LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-H)	81-108	303-339					
PRF32	HUMAN LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-M)	235-352						
PRF33	HUMAN LOW DENSITY LIPOPROTEIN RECEPTOR PRECURSOR	483-510						
PRF34	HUMAN A2ALGOLYCEPROTEIN RECEPTOR 1 (HEPATIC LECTIN HI) (ALGPR)	62-86						
PRF35	HUMAN 3-SELECTIN PRECURSOR (CELLULAR MEMBRANE PROTEIN 140) (CDP-140) (P40GEM)	32-59	83-114					
PRF36	HUMAN LACTOYLGLUTATHIONE LYASE (EC 4.4.1.3) (METHYLOXYALASE)	93-122						
PRF37	HUMAN LEUKAEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION)	153-179	233-263	298-336	671-698	974-991	1036-1066	
PRF38	HUMAN LING-1 REVERSE TRANSCRIPTASE HOMOLOG	154-183						
PRF39	HUMAN HORMONE SENSITIVE LIPASE (EC 3.1.1.3) (LIPASE, GASTRIC)	105-332						
PRF40	HUMAN LEUKOTRIENE A-4 HYDROLASE (EC 3.1.1.3) (HSL)	42-43	395-334					
PRF41	HUMAN LAMININ A1 CHAIN PRECURSOR	1318-1345	1741-1771	1785-1812	1824-1851	1864-1921	1965-1999	2091-2118
PRF42	HUMAN LAMININ B1 CHAIN PRECURSOR	1297-1314	1364-1394	1597-1631	1651-1714	1723-1781		
PRF43	HUMAN LAMININ B2 CHAIN PRECURSOR	1105-1133	1515-1542					
PRF44	HUMAN LAMININ B3 CHAIN PRECURSOR	153-182						
PRF45	HUMAN TYROSINE-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2)	341-366						
PRF46	HUMAN ALACIDONATE 12-LIPOXYGENASE (EC 1.13.11.3) (12-LOX)	50-87						
PRF47	HUMAN ALACIDONATE 12-LIPOXYGENASE (EC 1.13.11.3) (12-LOX)	776-803						
PRF48	HUMAN LACTASE PHLOUZIN HYDROLASE PRECURSOR (EC 3.1.1.18) (LACTASE)	108-1108						
PRF49	HUMAN PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (PTP-BETA)	108-1108						
PRF50	HUMAN PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48)	553-587	1024-1051	1973-2000				
PRF51	HUMAN PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR (EC 3.1.3.48) (PTP-ZETA)	46-114						
PRF52	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF53	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF54	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF55	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF56	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF57	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF58	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF59	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF60	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF61	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF62	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF63	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF64	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF65	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF66	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF67	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF68	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF69	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF70	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF71	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF72	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF73	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF74	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF75	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF76	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF77	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF78	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF79	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF80	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF81	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF82	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF83	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF84	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF85	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF86	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF87	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF88	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF89	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF90	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF91	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF92	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF93	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF94	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF95	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF96	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF97	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF98	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF99	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						
PRF100	HUMAN LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR PRECURSOR (LH/CG-R)	61-85						

Accession		Gene		Protein		Function		EC		Area 1		Area 2		Area 3		Area 4		Area 5		Area 6		Area 7		Area 8		Area 9		Area 10		Area 11		Area 12		Area 13		Area 14		Area 15		Area 16		Area 17		Area 18		Area 19		Area 20		Area 21		Area 22		Area 23		Area 24		Area 25		Area 26		Area 27		Area 28		Area 29		Area 30		Area 31		Area 32		Area 33		Area 34		Area 35		Area 36		Area 37		Area 38		Area 39		Area 40		Area 41		Area 42		Area 43		Area 44		Area 45		Area 46		Area 47		Area 48		Area 49		Area 50		Area 51		Area 52		Area 53		Area 54		Area 55		Area 56		Area 57		Area 58		Area 59		Area 60		Area 61		Area 62		Area 63		Area 64		Area 65		Area 66		Area 67		Area 68		Area 69		Area 70		Area 71		Area 72		Area 73		Area 74		Area 75		Area 76		Area 77		Area 78		Area 79		Area 80		Area 81		Area 82		Area 83		Area 84		Area 85		Area 86		Area 87		Area 88		Area 89		Area 90		Area 91		Area 92		Area 93		Area 94		Area 95		Area 96		Area 97		Area 98		Area 99		Area 100		Area 101		Area 102		Area 103		Area 104		Area 105		Area 106		Area 107		Area 108		Area 109		Area 110		Area 111		Area 112		Area 113		Area 114		Area 115		Area 116		Area 117		Area 118		Area 119		Area 120		Area 121		Area 122		Area 123		Area 124		Area 125		Area 126		Area 127		Area 128		Area 129		Area 130		Area 131		Area 132		Area 133		Area 134		Area 135		Area 136		Area 137		Area 138		Area 139		Area 140		Area 141		Area 142		Area 143		Area 144		Area 145		Area 146		Area 147		Area 148		Area 149		Area 150		Area 151		Area 152		Area 153		Area 154		Area 155		Area 156		Area 157		Area 158		Area 159		Area 160		Area 161		Area 162		Area 163		Area 164		Area 165		Area 166		Area 167		Area 168		Area 169		Area 170		Area 171		Area 172		Area 173		Area 174		Area 175		Area 176		Area 177		Area 178		Area 179		Area 180		Area 181		Area 182		Area 183		Area 184		Area 185		Area 186		Area 187		Area 188		Area 189		Area 190		Area 191		Area 192		Area 193		Area 194		Area 195		Area 196		Area 197		Area 198		Area 199		Area 200		Area 201		Area 202		Area 203		Area 204		Area 205		Area 206		Area 207		Area 208		Area 209		Area 210		Area 211		Area 212		Area 213		Area 214		Area 215		Area 216		Area 217		Area 218		Area 219		Area 220		Area 221		Area 222		Area 223		Area 224		Area 225		Area 226		Area 227		Area 228		Area 229		Area 230		Area 231		Area 232		Area 233		Area 234		Area 235		Area 236		Area 237		Area 238		Area 239		Area 240		Area 241		Area 242		Area 243		Area 244		Area 245		Area 246		Area 247		Area 248		Area 249		Area 250		Area 251		Area 252		Area 253		Area 254		Area 255		Area 256		Area 257		Area 258		Area 259		Area 260		Area 261		Area 262		Area 263		Area 264		Area 265		Area 266		Area 267		Area 268		Area 269		Area 270		Area 271		Area 272		Area 273		Area 274		Area 275		Area 276		Area 277		Area 278		Area 279		Area 280		Area 281		Area 282		Area 283		Area 284		Area 285		Area 286		Area 287		Area 288		Area 289		Area 290		Area 291		Area 292		Area 293		Area 294		Area 295		Area 296		Area 297		Area 298		Area 299		Area 300		Area 301		Area 302		Area 303		Area 304		Area 305		Area 306		Area 307		Area 308		Area 309		Area 310		Area 311		Area 312		Area 313		Area 314		Area 315		Area 316		Area 317		Area 318		Area 319		Area 320		Area 321		Area 322		Area 323		Area 324		Area 325		Area 326		Area 327		Area 328		Area 329		Area 330		Area 331		Area 332		Area 333		Area 334		Area 335		Area 336		Area 337		Area 338		Area 339		Area 340		Area 341		Area 342		Area 343		Area 344		Area 345		Area 346		Area 347		Area 348		Area 349		Area 350		Area 351		Area 352		Area 353		Area 354		Area 355		Area 356		Area 357		Area 358		Area 359		Area 360		Area 361		Area 362		Area 363		Area 364		Area 365		Area 366		Area 367		Area 368		Area 369		Area 370		Area 371		Area 372		Area 373		Area 374		Area 375		Area 376		Area 377		Area 378		Area 379		Area 380		Area 381		Area 382		Area 383		Area 384		Area 385		Area 386		Area 387		Area 388		Area 389		Area 390		Area 391		Area 392		Area 393		Area 394		Area 395		Area 396		Area 397		Area 398		Area 399		Area 400		Area 401		Area 402		Area 403		Area 404		Area 405		Area 406		Area 407		Area 408		Area 409		Area 410		Area 411		Area 412		Area 413		Area 414		Area 415		Area 416		Area 417		Area 418		Area 419		Area 420		Area 421		Area 422		Area 423		Area 424		Area 425		Area 426		Area 427		Area 428		Area 429		Area 430		Area 431		Area 432		Area 433		Area 434		Area 435		Area 436		Area 437		Area 438		Area 439		Area 440		Area 441		Area 442		Area 443		Area 444		Area 445		Area 446		Area 447		Area 448		Area 449		Area 450		Area 451		Area 452		Area 453		Area 454		Area 455		Area 456		Area 457		Area 458		Area 459		Area 460		Area 461		Area 462		Area 463		Area 464		Area 465		Area 466		Area 467		Area 468		Area 469		Area 470		Area 471		Area 472		Area 473		Area 474		Area 475		Area 476		Area 477		Area 478		Area 479		Area 480		Area 481		Area 482		Area 483		Area 484		Area 485		Area 486		Area 487		Area 488		Area 489		Area 490		Area 491		Area 492		Area 493		Area 494		Area 495		Area 496		Area 497		Area 498		Area 499		Area 500		Area 501		Area 502		Area 503		Area 504		Area 505		Area 506		Area 507		Area 508		Area 509		Area 510		Area 511		Area 512		Area 513		Area 514		Area 515		Area 516		Area 517		Area 518		Area 519		Area 520		Area 521		Area 522		Area 523		Area 524		Area 525		Area 526		Area 527		Area 528		Area 529		Area 530		Area 531		Area 532		Area 533		Area 534		Area 535		Area 536		Area 537		Area 538		Area 539		Area 540		Area 541		Area 542		Area 543		Area 544		Area 545		Area 546		Area 547		Area 548		Area 549		Area 550		Area 551		Area 552		Area 553		Area 554		Area 555		Area 556		Area 557		Area 558		Area 559		Area 560		Area 561		Area 562		Area 563		Area 564		Area 565		Area 566		Area 567		Area 568		Area 569		Area 570		Area 571		Area 572		Area 573		Area 574		Area 575		Area 576		Area 577		Area 578		Area 579		Area 580		Area 581		Area 582		Area 583		Area 584		Area 585		Area 586		Area 587		Area 588		Area 589		Area 590		Area 591		Area 592		Area 593		Area 594		Area 595		Area 596		Area 597		Area 598		Area 599		Area 600		Area 601		Area 602		Area 603		Area 604		Area 605		Area 606		Area 607		Area 608		Area 609		Area 610		Area 611		Area 612		Area 613		Area 614		Area 615		Area 616		Area 617		Area 618		Area 619		Area 620		Area 621		Area 622		Area 623		Area 624		Area 625		Area 626		Area 627		Area 628		Area 629		Area 630		Area 631		Area 632		Area 633		Area 634		Area 635		Area 636		Area 637		Area 638		Area 639		Area 640		Area 641		Area 642		Area 643		Area 644		Area 645		Area 646		Area 647		Area 648		Area 649		Area 650		Area 651		Area 652		Area 653		Area 654		Area 655		Area 656		Area 657		Area 658		Area 659		Area 660		Area 661		Area 662		Area 663		Area 664		Area 665		Area 666		Area 667		Area 668		Area 669		Area 670		Area 671		Area 672		Area 673		Area 674		Area 675		Area 676		Area 677		Area 678		Area 679		Area 680		Area 681		Area 682		Area 683		Area 684		Area 685		Area 686		Area 687		Area 688		Area 689		Area 690		Area 691		Area 692		Area 693		Area 694		Area 695		Area 696		Area 697		Area 698		Area 699		Area 700		Area 701		Area 702		Area 703		Area 704		Area 705		Area 706		Area 707		Area 708		Area 709		Area 710		Area 711		Area 712		Area 713		Area 714		Area 715		Area 716		Area 717		Area 718		Area 719		Area 720		Area 721		Area 722		Area 723		Area 724		Area 725		Area 726		Area 727		Area 728		Area 729		Area 730		Area 731		Area 732		Area 733		Area 734		Area 735		Area 736		Area 737		Area 738		Area 739		Area 740		Area 741		Area 742		Area 743		Area 744		Area 745		Area 746		Area 747		Area 748		Area 749		Area 750		Area 751		Area 752		Area 753		Area 754		Area 755		Area 756		Area 757		Area 758		Area 759		Area 760		Area 761		Area 762		Area 763		Area 764		Area 765		Area 766		Area 767		Area 768		Area 769		Area 770		Area 771		Area 772		Area 773		Area 774		Area 775		Area 776		Area 777		Area 778		Area 779		Area 780		Area 781		Area 782		Area 783		Area 784		Area 785		Area 786		Area 787		Area 788		Area 789		Area 790		Area 791		Area 792		Area 793		Area 794		Area 795		Area 796		Area 797		Area 798		Area 799		Area 800		Area 801		Area 802		Area 803		Area 804		Area 805		Area 806		Area 807		Area 808		Area 809		Area 810		Area 811		Area 812		Area 813		Area 814		Area 815		Area 816		Area 817		Area 818		Area 819		Area 820		Area 821		Area 822		Area 823		Area 824		Area 825		Area 826		Area 827		Area 828		Area 829		Area 830		Area 831		Area 832		Area 833		Area 834		Area 835		Area 836		Area 837		Area 838		Area 839		Area 840		Area 841		Area 842		Area 843		Area 844		Area 845		Area 846		Area 847		Area 848		Area 849		Area 850		Area 851		Area 852		Area 853		Area 854		Area 855		Area 856		Area 857		Area 858		Area 859		Area 860		Area 861		Area 862		Area 863		Area 864		Area 865		Area 866		Area 867		Area 868		Area 869		Area 870		Area 871		Area 872		Area 873		Area 874		Area 875		Area 876		Area 877		Area 878		Area 879		Area 880		Area 881		Area 882		Area 883		Area 884		Area 885		Area 886		Area 887		Area 888		Area 889		Area 890		Area 891		Area 892		Area 893		Area 894		Area 895		Area 896		Area 897		Area 898		Area 899		Area 900		Area 901		Area 902		Area 903		Area 904		Area 905		Area 906		Area 907		Area 908		Area 909		Area 910		Area 911		Area 912		Area 913		Area 914		Area 915		Area 916		Area 917		Area 918		Area 919		Area 920		Area 921		Area 922		Area 923		Area 924		Area 925		Area 926		Area 927		Area 928		Area 929		Area 930		Area 931		Area 932		Area 933		Area 934		Area 935		Area 936		Area 937		Area 938		Area 939		Area 940		Area 941		Area 942		Area 943		Area 944		Area 945		Area 946		Area 947		Area 948		Area 949		Area 950		Area 951		Area 952		Area 953		Area 954		Area 955		Area 956		Area 957	
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EC/ENZYME	1971-1984 Nomenclature as All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PLA2	PHOSPHATIDYLPHOSPHOLIPASE 2	142-169	319-366							
PLA2	PLACLOLOBIN (DESMOPHILIN III)	171-400								
PLA2	PLASTIN (SUBUNIT)	507-524								
PLA2	PLASTIN 1 (SUBUNIT)	510-541								
PLA2	PLASTIN 2 (SUBUNIT)	511-541								
PLA2	PLASTIN 3 (SUBUNIT)	512-541								
PLA2	PLASTIN 4 (SUBUNIT)	513-541								
PLA2	PLASTIN 5 (SUBUNIT)	514-541								
PLA2	PLASTIN 6 (SUBUNIT)	515-541								
PLA2	PLASTIN 7 (SUBUNIT)	516-541								
PLA2	PLASTIN 8 (SUBUNIT)	517-541								
PLA2	PLASTIN 9 (SUBUNIT)	518-541								
PLA2	PLASTIN 10 (SUBUNIT)	519-541								
PLA2	PLASTIN 11 (SUBUNIT)	520-541								
PLA2	PLASTIN 12 (SUBUNIT)	521-541								
PLA2	PLASTIN 13 (SUBUNIT)	522-541								
PLA2	PLASTIN 14 (SUBUNIT)	523-541								
PLA2	PLASTIN 15 (SUBUNIT)	524-541								
PLA2	PLASTIN 16 (SUBUNIT)	525-541								
PLA2	PLASTIN 17 (SUBUNIT)	526-541								
PLA2	PLASTIN 18 (SUBUNIT)	527-541								
PLA2	PLASTIN 19 (SUBUNIT)	528-541								
PLA2	PLASTIN 20 (SUBUNIT)	529-541								
PLA2	PLASTIN 21 (SUBUNIT)	530-541								
PLA2	PLASTIN 22 (SUBUNIT)	531-541								
PLA2	PLASTIN 23 (SUBUNIT)	532-541								
PLA2	PLASTIN 24 (SUBUNIT)	533-541								
PLA2	PLASTIN 25 (SUBUNIT)	534-541								
PLA2	PLASTIN 26 (SUBUNIT)	535-541								
PLA2	PLASTIN 27 (SUBUNIT)	536-541								
PLA2	PLASTIN 28 (SUBUNIT)	537-541								
PLA2	PLASTIN 29 (SUBUNIT)	538-541								
PLA2	PLASTIN 30 (SUBUNIT)	539-541								
PLA2	PLASTIN 31 (SUBUNIT)	540-541								
PLA2	PLASTIN 32 (SUBUNIT)	541-541								
PLA2	PLASTIN 33 (SUBUNIT)	542-541								
PLA2	PLASTIN 34 (SUBUNIT)	543-541								
PLA2	PLASTIN 35 (SUBUNIT)	544-541								
PLA2	PLASTIN 36 (SUBUNIT)	545-541								
PLA2	PLASTIN 37 (SUBUNIT)	546-541								
PLA2	PLASTIN 38 (SUBUNIT)	547-541								
PLA2	PLASTIN 39 (SUBUNIT)	548-541								
PLA2	PLASTIN 40 (SUBUNIT)	549-541								
PLA2	PLASTIN 41 (SUBUNIT)	550-541								
PLA2	PLASTIN 42 (SUBUNIT)	551-541								
PLA2	PLASTIN 43 (SUBUNIT)	552-541								
PLA2	PLASTIN 44 (SUBUNIT)	553-541								
PLA2	PLASTIN 45 (SUBUNIT)	554-541								
PLA2	PLASTIN 46 (SUBUNIT)	555-541								
PLA2	PLASTIN 47 (SUBUNIT)	556-541								
PLA2	PLASTIN 48 (SUBUNIT)	557-541								
PLA2	PLASTIN 49 (SUBUNIT)	558-541								
PLA2	PLASTIN 50 (SUBUNIT)	559-541								
PLA2	PLASTIN 51 (SUBUNIT)	560-541								
PLA2	PLASTIN 52 (SUBUNIT)	561-541								
PLA2	PLASTIN 53 (SUBUNIT)	562-541								
PLA2	PLASTIN 54 (SUBUNIT)	563-541								
PLA2	PLASTIN 55 (SUBUNIT)	564-541								
PLA2	PLASTIN 56 (SUBUNIT)	565-541								
PLA2	PLASTIN 57 (SUBUNIT)	566-541								
PLA2	PLASTIN 58 (SUBUNIT)	567-541								
PLA2	PLASTIN 59 (SUBUNIT)	568-541								
PLA2	PLASTIN 60 (SUBUNIT)	569-541								
PLA2	PLASTIN 61 (SUBUNIT)	570-541								
PLA2	PLASTIN 62 (SUBUNIT)	571-541								
PLA2	PLASTIN 63 (SUBUNIT)	572-541								
PLA2	PLASTIN 64 (SUBUNIT)	573-541								
PLA2	PLASTIN 65 (SUBUNIT)	574-541								
PLA2	PLASTIN 66 (SUBUNIT)	575-541								
PLA2	PLASTIN 67 (SUBUNIT)	576-541								
PLA2	PLASTIN 68 (SUBUNIT)	577-541								
PLA2	PLASTIN 69 (SUBUNIT)	578-541								
PLA2	PLASTIN 70 (SUBUNIT)	579-541								
PLA2	PLASTIN 71 (SUBUNIT)	580-541								
PLA2	PLASTIN 72 (SUBUNIT)	581-541								
PLA2	PLASTIN 73 (SUBUNIT)	582-541								
PLA2	PLASTIN 74 (SUBUNIT)	583-541								
PLA2	PLASTIN 75 (SUBUNIT)	584-541								
PLA2	PLASTIN 76 (SUBUNIT)	585-541								
PLA2	PLASTIN 77 (SUBUNIT)	586-541								
PLA2	PLASTIN 78 (SUBUNIT)	587-541								
PLA2	PLASTIN 79 (SUBUNIT)	588-541								
PLA2	PLASTIN 80 (SUBUNIT)	589-541								
PLA2	PLASTIN 81 (SUBUNIT)	590-541								
PLA2	PLASTIN 82 (SUBUNIT)	591-541								
PLA2	PLASTIN 83 (SUBUNIT)	592-541								
PLA2	PLASTIN 84 (SUBUNIT)	593-541								
PLA2	PLASTIN 85 (SUBUNIT)	594-541								
PLA2	PLASTIN 86 (SUBUNIT)	595-541								
PLA2	PLASTIN 87 (SUBUNIT)	596-541								
PLA2	PLASTIN 88 (SUBUNIT)	597-541								
PLA2	PLASTIN 89 (SUBUNIT)	598-541								
PLA2	PLASTIN 90 (SUBUNIT)	599-541								
PLA2	PLASTIN 91 (SUBUNIT)	600-541								
PLA2	PLASTIN 92 (SUBUNIT)	601-541								
PLA2	PLASTIN 93 (SUBUNIT)	602-541								
PLA2	PLASTIN 94 (SUBUNIT)	603-541								
PLA2	PLASTIN 95 (SUBUNIT)	604-541								
PLA2	PLASTIN 96 (SUBUNIT)	605-541								
PLA2	PLASTIN 97 (SUBUNIT)	606-541								
PLA2	PLASTIN 98 (SUBUNIT)	607-541								
PLA2	PLASTIN 99 (SUBUNIT)	608-541								
PLA2	PLASTIN 100 (SUBUNIT)	609-541								
PLA2	PLASTIN 101 (SUBUNIT)	610-541								
PLA2	PLASTIN 102 (SUBUNIT)	611-541								
PLA2	PLASTIN 103 (SUBUNIT)	612-541								
PLA2	PLASTIN 104 (SUBUNIT)	613-541								
PLA2	PLASTIN 105 (SUBUNIT)	614-541								
PLA2	PLASTIN 106 (SUBUNIT)	615-541								
PLA2	PLASTIN 107 (SUBUNIT)	616-541								
PLA2	PLASTIN 108 (SUBUNIT)	617-541								
PLA2	PLASTIN 109 (SUBUNIT)	618-541								
PLA2	PLASTIN 110 (SUBUNIT)	619-541								
PLA2	PLASTIN 111 (SUBUNIT)	620-541								
PLA2	PLASTIN 112 (SUBUNIT)	621-541								
PLA2	PLASTIN 113 (SUBUNIT)	622-541								
PLA2	PLASTIN 114 (SUBUNIT)	623-541								
PLA2	PLASTIN 115 (SUBUNIT)	624-541								
PLA2	PLASTIN 116 (SUBUNIT)	625-541								
PLA2	PLASTIN 117 (SUBUNIT)	626-541								
PLA2	PLASTIN 118 (SUBUNIT)	627-541								
PLA2	PLASTIN 119 (SUBUNIT)	628-541								
PLA2	PLASTIN 120 (SUBUNIT)	629-541								
PLA2	PLASTIN 121 (SUBUNIT)	630-541								
PLA2	PLASTIN 122 (SUBUNIT)	631-541								
PLA2	PLASTIN 123 (SUBUNIT)	632-541								
PLA2	PLASTIN 124 (SUBUNIT)	633-541								
PLA2	PLASTIN 125 (SUBUNIT)	634-541								
PLA2	PLASTIN 126 (SUBUNIT)	635-541								
PLA2	PLASTIN 127 (SUBUNIT)	636-541								
PLA2	PLASTIN 128 (SUBUNIT)	637-541								
PLA2	PLASTIN 129 (SUBUNIT)	638-541								
PLA2	PLASTIN 130 (SUBUNIT)	639-541								
PLA2	PLASTIN 131 (SUBUNIT)	640-541								
PLA2	PLASTIN 132 (SUBUNIT)	641-541								
PLA2	PLASTIN 133 (SUBUNIT)	642-541								
PLA2	PLASTIN 134 (SUBUNIT)	643-541								
PLA2	PLASTIN 135 (SUBUNIT)	644-541								
PLA2	PLASTIN 136 (SUBUNIT)	645-541								
PLA2	PLASTIN 137 (SUBUNIT)	646-541								
PLA2	PLASTIN 138 (SUBUNIT)	647-541								
PLA2	PLASTIN 139 (SUBUNIT)	648-541								
PLA2	PLASTIN 140 (SUBUNIT)	649-541								
PLA2	PLASTIN 141 (SUBUNIT)	650-541								
PLA2	PLASTIN 142 (SUBUNIT)	651-541								
PLA2	PLASTIN 143 (SUBUNIT)	652-541								
PLA2	PLASTIN 144 (SUBUNIT)	653-541								
PLA2	PLASTIN 145 (SUBUNIT)	654-541								
PLA2	PLASTIN 146 (SUBUNIT)	655-541								
PLA2	PLASTIN 147 (SUBUNIT)	656-541								
PLA2	PLASTIN 148 (SUBUNIT)	657-541								
PLA2	PLASTIN 149 (SUBUNIT)	658-541								
PLA2	PLASTIN 150 (SUBUNIT)	659-541								
PLA2	PLASTIN 151 (SUBUNIT)	660-541								
PLA2	PLASTIN 152 (SUBUNIT)	661-541								
PLA2	PLASTIN 153 (SUBUNIT)	662-541								
PLA2	PLASTIN 154 (SUBUNIT)	663-541								
PLA2	PLASTIN 155 (SUBUNIT)	664-541								
PLA2	PLASTIN 156 (SUBUNIT)	665-541								
PLA2	PLASTIN 157 (SUBUNIT)	666-541								
PLA2	PLASTIN 158 (SUBUNIT)	667-541								
PLA2	PLASTIN 159 (SUBUNIT)	668-541								
PLA2	PLASTIN 160 (SUBUNIT)	669-541								
PLA2	PLASTIN 161 (SUBUNIT)	670-541								
PLA2	PLASTIN 162 (SUBUNIT)	671-541								
PLA2	PLASTIN 163 (SUBUNIT)	672-541								
PLA2	PLASTIN 164 (SUBUNIT)	673-541								
PLA2	PLASTIN 165 (SUBUNIT)	674-541								

PGCONE	(1971)1st Medl Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10
PALP HUMAN	40S RIBOSOMAL PROTEIN L9	146-193									
PALAO HUMAN	40S ACIDIC RIBOSOMAL PROTEIN P0 (L10)	131-165									
PROS1 HUMAN	31 KD PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (S1-A))	190-233	318-265								
PROS2 HUMAN	60 KD PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (S2-A))	192-245									
PROS3 HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C1 AND HNRNP	18-43									
PROL HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN L (HNRPL)	301-338									
PROU HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN U	635-657									
PRP81 HUMAN	RNA-DIRECTED RNA POLYMERASE II 315 KD POLYPEPTIDE	338-394	665-720	1008-1015	1371-1395						
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	614-667	1008-1015								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	242-274									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	318-353									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	378-405									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	396-423									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	60-87									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	89-116									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	26-53									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	14-41									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	73-100									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	116-161									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	121-150									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	13-47									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	17-44									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	154-188	445-522	2020-2847	3104-3331	3329-3356	3912-3919	4021-4048			
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	12-34									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	14-56									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	31-38									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	389-416									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	700-736									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	34-101									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	64-81	176-226	334-368							
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	71-98	193-226	403-439	539-573						
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	38-45	154-181								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	146-178									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	336-381	390-337	514-541							
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	84-113	153-193	216-231							
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	331-358	545-572								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	414-441									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	193-220	570-621	1009-1136	1461-1502	1832-1909	1918-2022	2120-2134	2223-2350		
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	3346-3373									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	150-177	316-350	466-520	987-1021	1037-1083	1287-1324	1347-1374	1834-1861		
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	90-124									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	77-104	480-507								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	76-110									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	389-318									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	67-74									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	1748-1753									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	31-47									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	44-71									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	174-201	740-771								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	380-442	468-502								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	140-167	230-277								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	495-524	618-645								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	230-237	413-440								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	93-137	196-233								
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	34-48									
PRP83 HUMAN	RNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	169-196	245-272								

PCGENE	19717144 Nucleotide Sequence on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PIA1	PROTEIN									
PIA2	TRANSCRIPTION FACTOR JUN-B	296-323								
PIA3	TRANSCRIPTION FACTOR JUN-D	291-333								
PIA4	MICROTUBULE-ASSOCIATED PROTEIN TAU	279-303								
PIA5	MICROTUBULE-ASSOCIATED PROTEIN TAU, FETAL	211-228								
PIB1	TRANSCOBALANIN PRECURSOR	201-241	330-337							
PIB2	T-COMPLEX PROTEIN 1 (TCP-1)	318-343								
PIB3	RNA NUCLEOTIDYLTRANSFERASE (EC 2.7.7.1) (TERMINAL ADDITION NUCLEOTIDYLTRANSFERASE)	61-93								
PIB4	RECEPTOR TYROSINE KINASE TEK PRECURSOR (EC 2.7.1.13) (TK-6)	144-278	260-296	1003-1016						
PIB5	TRANSCRIPTION INITIATION FACTOR IIB (TFIID)	133-162								
PIB6	TRANSCRIPTION FACTOR E3 (FRAGMENT)	43-70	172-149	178-226						
PIB7	TRANSCRIPTION ELONGATION FACTOR 3-II	35-56								
PIB8	TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)	148-175								
PIB9	TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1)	148-183								
PIB10	TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2) (HILHILANTII)	145-170								
PIB11	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (ECF-LIKE TGF)	87-114								
PIB12	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K (EC 2.3.3.1)	338-385								
PIB13	THROMBOSPONDIN PRECURSOR	110-163	384-314							
PIB14	3-BETAOXY-COA THIOLEASE PEROXISOMAL PRECURSOR (EC 2.3.1.16) (BETA-3-OXY-COA THIOLEASE)	183-212								
PIB15	PROTEIN KINASE C (PKC) PRECURSOR (CONTAINS SUBSTANCE P NEUROKININ A)	11-38								
PIB16	TRANSDUCIN-LIKE ENHANCER PROTEIN 1	616-653								
PIB17	TRANSDUCIN-LIKE ENHANCER PROTEIN 2	94-123								
PIB18	TRANSDUCIN-LIKE ENHANCER PROTEIN 4 (FRAGMENT)	304-331								
PIB19	RNA TOPOISOMERASE II, ALPHA ISOZYME (EC 5.99.1.2)	19-46	503-532							
PIB20	RNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3)	33-63	616-647							
PIB21	TROPOMYOSIN, FIBROBLAST (SOFORIN TM)	16-74	82-116							
PIB22	TROPOMYOSIN, ALPHA CHAIN, SKELETAL MUSCLE	16-41	42-74	32-116	191-237	243-277				
PIB23	TROPOMYOSIN, BETA CHAIN, SKELETAL MUSCLE	33-116	193-240							
PIB24	TROPOMYOSIN, CARDIAC MUSCLE	16-74	82-116	193-237						
PIB25	TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TK16) (TIME1)	37-116	210-240	243-270						
PIB26	TROPOMYOSIN, FIBROBLAST NON-MUSCLE TYPE (TM10PL)	46-80	111-138	138-166	207-234					
PIB27	TROPOMYOSIN, CYTOSKELETAL TYPE (TM10NL)	46-80	111-138	172-199						
PIB28	TROPOMYOSIN, ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT)	31-59	147-178							
PIB29	TROPOMYOSIN, ALPHA CHAIN, SMOOTH MUSCLE (FRAGMENT)	31-59	147-178							
PIB30	TRYPTEPTIDYL-PEPTIDASE II (EC 3.4.11.10) (TPP-II) (TRYPTEPTIDYL-PEPTIDASE II)	133-183	1008-1031	1160-1187						
PIB31	TPK ONCOGENE (FRAGMENT)	82-147								
PIB32	TREMBL PROTEIN	18-43	342-269							
PIB33	THYROTROPIN-RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBERIN RECEPTOR)	149-353								
PIB34	TROPOMYOSIN, CARDIAC MUSCLE	16-41								
PIB35	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.12)	66-93	117-148							
PIB36	THYROTROPIN RECEPTOR PROTEIN (TR) (ANTIGEN CD11) (TV)	188-215	364-393							
PIB37	THYROTROPIN RECEPTOR PRECURSOR (TSH-R)	87-117	428-447							
PIB38	PROTEIN KINASE TKK (EC 2.7.1.1)	170-197	324-339	310-344	349-381					
PIB39	NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.113)	159-177								
PIB40	UBIQUITIN-ACTIVATING ENZYME E1 (U1) (PROTEIN)	448-475								
PIB41	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)	227-334								
PIB42	UDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MICROSMAL (EC 2.4.1.17)	227-334								
PIB43	RECEPTOR TYROSINE-PROTEIN KINASE UFO PRECURSOR (EC 2.7.1.113)	488-522								
PIB44	UPSTREAM STIMULATORY FACTOR 1	251-295								
PIB45	VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)	47-74	117-147							
PIB46	VILIN	338-372	437-461	717-744						
PIB47	VIMENTIN	118-148	233-260							
PIB48	VINCULIN	109-135								
PIB49	RETROVIRUS-RELATED PROTEINASE (EC 3.4.21.-)	93-114								
PIB50	WEEL-LIKE PROTEIN KINASE (EC 2.7.1.112)	354-388								
PIB51	WILMS TUMOR PROTEIN (WT3)	247-274								
PIB52	X-BOX BINDING PROTEIN-1 (XBP-1) (XBP1 PROTEIN)	97-115								
PIB53	X-BOX BINDING PROTEIN-2 (XBP-2) (XBP2 PROTEIN)	180-211								
PIB54	DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS (XERODERMA PIGMENTOSUM XP-A)	101-128								
PIB55	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM XP-C)	101-128								

PCGENE	1071171.4 Medit Search on All Human Protein Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
FILE NAME	PROTEIN	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
P20C HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM) [24-29]	115-166	1047-1081							
P20C HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM) [11-110]									
P20C HUMAN	DNA-REPAIR PROTEIN XPGC1	23-37								
P20C HUMAN	DNA-REPAIR PROTEIN XPGC1	29-36								
P210 HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN K0X1) (FRAGMENT)	12-43	107-114	1071-1078	1409-1500	2011-2017	2146-2180			
P210 HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER)	3-30	201-228							
P2M3 HUMAN	ZINC FINGER PROTEIN 43 (ZRC1744) (FRAGMENT)									
P2M6 HUMAN	ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KLP)	131-149								

TABLE X

**Search Results Summary for PCTLZIP,
P1CTLZIP, and P2CTLZIP Motifs**

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PHEMA MUMPM	133-148							PHEMA LABAN	221-237				PHEMA GPHOC	301-408
PHEMA MUMPR	133-148							PHEMA LABUD	234-260				PHEMA IALIC	322-338
PHEMA MUMPB	133-148							PHEMA IACKA	234-260				PHEMA IABAN	306-323
PHEMA P11HW	345-360							PHEMA IACKO	231-247				PHEMA IABUD	320-337
PHEMA P12H	65-80							PHEMA IACKV	230-246				PHEMA IACKA	320-337
PHEMA P12HT	65-80							PHEMA IADA1	234-260				PHEMA IACKO	316-333
PHEMA RINDK	308-383							PHEMA IADA3	237-263				PHEMA IACKP	303-319
PHEMA SVS	7-84							PHEMA IADCE	234-260				PHEMA IACKO	302-318
PHEMA SVSCM	7-84							PHEMA IADH1	221-237				PHEMA IACKV	319-336
PHEMA SVSCP	7-84							PHEMA IADH2	221-237				PHEMA IACKB	316-332
PHEMA SVGLN	7-84							PHEMA IADH3	221-237				PHEMA IADAY	320-337
PVENV D1V11	42-57							PHEMA IADH4	221-237				PHEMA IADH1	322-339
PVP77 CAPYK	60-104							PHEMA IADH6	221-237				PHEMA IADCE	320-337
PVJUS VACC0	72-87							PHEMA IADH7	221-237				PHEMA IADH1	306-323
PV001 BPP22	242-267							PHEMA IADH2	221-237				PHEMA IADH2	306-323
PV001 HBVEB	189-184							PHEMA IADH2	237-263				PHEMA IADH3	306-323
PV001 HBV11	210-226							PHEMA IADH2	234-260				PHEMA IADH4	306-323
PV006 BPT4	184-199							PHEMA IADH6	221-237				PHEMA IADH6	306-323
PV007 BPT4	685-900							PHEMA IADH7	237-263				PHEMA IADH7	306-323
PV008 HBV11	134-149							PHEMA IADH7	237-263				PHEMA IADH7	306-323
PV010 BPPH2	183-198							PHEMA IADH7	230-246				PHEMA IADH2	322-339
PV010 BPPZA	183-198							PHEMA IADH7	230-246				PHEMA IADH3	322-339
PV010 HBV8A	109-124							PHEMA IADH7	230-246				PHEMA IADH3	306-323
PV016 BPP1	181-86							PHEMA IADH7	230-246				PHEMA IADH4	306-323
PV016 BPT4	468-483							PHEMA IADH7	230-246				PHEMA IADH6	306-323
PV026 BPT4	87-112							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV029 HBV11	20-38							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV030 BPPH8	11-84							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV036 BPOX2	22-37							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV036 HBV8A	109-123							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV037 BPT2	1263-1268							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV037 HBV11	284-289							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV055 HBV11	22-37							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV055 HBV11	268-283							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV088 HBV11	103-117							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV088 HBV11	287-282							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV085 HBV11	619-633							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV08 BPPH2	234-249							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV08 BPPZA	234-240							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV09 BPPV1R	67-72							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0F BPPHX	234-240							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVBF	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVL6	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVBLV	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVBM	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVBQ	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323
PV0L2 CVBV	284-278							PHEMA IADH7	230-246				PHEMA IADH7	306-323

PVGL3 CVPF5	442-457		PHEMA IAME6	231-237			PHEMA IAHTO	321-338
PVGL3 CVPF6	440-455	604-619	PHEMA IAMIN	86-101	231-247		PHEMA IAHUR	321-338
PVGL3 CVPF8	218-233		PHEMA IANT6	237-253			PHEMA IAJAP	317-334
PVGL3 CVPF9	218-233		PHEMA IADU7	221-237			PHEMA IAMAA	318-336
PVGL3 IBV6	1086-1071		PHEMA IARUD	234-250			PHEMA IAMAB	324-341
PVGL3 IBV8	1085-1070		PHEMA IASE2	234-250			PHEMA IAMAO	322-338
PVGL3 IBVD2	1086-1071		PHEMA IASH2	234-250			PHEMA IAME1	322-338
PVGL3 IBV4	1085-1070		PHEMA IASTA	230-246			PHEMA IAME2	322-338
PVGL3 IBVM	1085-1070		PHEMA IATAI	235-251			PHEMA IAME6	308-323
PVGL3 HBVA	701-716		PHEMA IATKM	234-250			PHEMA IAMIN	318-333
PVGL3 PRVIF	203-218		PHEMA IATKO	233-249			PHEMA IANT6	322-338
PVGL3 HBVC	476-490		PHEMA IATKR	230-246			PHEMA IAPIL	320-337
PVGL3 HBVE4	444-459		PHEMA IATKW	229-245			PHEMA IARUD	308-323
PVGL3 HBVE8	427-442		PHEMA IAUO	237-253			PHEMA IASE2	320-337
PVGL3 PRVIF	440-461		PHEMA IAU89	235-251			PHEMA IASH2	321-338
PVGL3 HBV11	78-84		PHEMA IAV7	236-254			PHEMA IASTA	316-332
PVGL3 HBV2	78-84		PHEMA IAXIA	235-251			PHEMA IATKM	320-337
PVGL3 HBVA	288-280		PHEMA IAZCO	237-253			PHEMA IAUO	322-338
PVGL3 HBVC	288-280		PHEMA IAZH2	221-237			PHEMA IAV7	323-340
PVGL3 HBVR	288-280		PHEMA IAZH3	221-237			PHEMA IAZCO	322-338
PVGL3 HBV1	288-280		PHEMA IAZUK	237-253			PHEMA IAZH2	308-323
PVGL3 HBVA	288-280		PHEMA INBAA	116-131	206-310		PHEMA IAZH3	308-323
PVGL3 HBVL	288-280		PHEMA INBBE	123-139	203-318		PHEMA IAZUK	322-338
PVGL3 HBVR	288-280		PHEMA INBBO	116-132	203-308		PHEMA MUMPM	101-116
PVGL3 MUMPS	6-94		PHEMA INBEN	123-139	301-316		PHEMA MUMPR	101-116
PVGL3 VZVD	278-293		PHEMA INBFU	108-124	206-301		PHEMA MUMPS	101-116
PVGLM HANTB	900-815		PHEMA INBOL	119-136	208-311		PHEMA NDVA	93-110
PVGLM PTPV	743-758		PHEMA INBHK	116-132	203-308		PHEMA NDVB	93-110
PVGLM SEOUR	801-816		PHEMA INBIB	108-124	206-303		PHEMA NDVH	93-110
PVGLM SEOUR	800-815		PHEMA INBID	120-136	206-314		PHEMA NDVI	93-110
PVGLY LABBQ	426-441		PHEMA INBLE	123-139	302-317		PHEMA NDVM	93-110
PVGLY LABBJ	427-442		PHEMA INBMD	113-126	202-307		PHEMA NDVM	93-110
PVGLY MOPEI	426-440		PHEMA INBME	110-132	206-311		PHEMA NDVQ	93-110
PVM3 REOVD	821-836		PHEMA INBNA	108-124	208-303		PHEMA NDVQ	93-110
PVMSA HPB08	380-395		PHEMA INBOR	123-139	301-316		PHEMA NDVU	93-110
PVMSA HPBV8	187-202		PHEMA INBBI	123-139	301-316		PHEMA PHODV	30-53
PVMSA WHV1	378-393		PHEMA INBSJ	119-136	206-313		PHEMA PIHW	486-503
PVMSA WHV69	383-398		PHEMA INBUS	116-132	204-308		PHEMA PI3B	111-128
PVMSA WHV7	383-398		PHEMA INBVI	110-132	206-311		PHEMA PI3H4	111-128
PVMSA WHV8	383-398		PHEMA INBVK	123-139	302-318		PHEMA PI3HA	111-128
PVMSA WHV81	383-398		PHEMA INBY8	108-124	206-301		PHEMA PI3HT	111-128
PVMSA WHVW6	234-246		PHEMA MUMPM	133-148			PHEMA PI3HU	111-128
PVMT3 IAJIN	28-40		PHEMA MUMPR	133-148			PHEMA PI3HV	111-128
PVMT3 IAGAN	26-40		PHEMA MUMPS	133-148			PHEMA PI3HW	111-128
PVMT3 IATOW	26-40		PHEMA PI1HW	346-360			PHEMA PI3HX	111-128
PVMT3 IAPPR	26-40		PHEMA PI2H	68-81			PHEMA PI3HA	60-67
PVMT3 IAPFW	28-40		PHEMA PI2HT	68-81				

PVMT2 IALE1	25-40		PIEMA PIB	324-340		PIEMA SV41	85-102
PVMT2 IALE2	25-40		PIEMA PIBA	324-340		PIEMA SV6	84-101
PVMT2 IAMAN	25-40		PIEMA PIBHA	324-340		PIEMA SV6CM	84-101
PVMT2 IAPUE	25-40		PIEMA PIBHT	324-340		PIEMA SVBCP	84-101
PVMT2 IABIN	25-40		PIEMA PIBHV	324-340		PIEMA SVELN	84-101
PVMT2 IAUDD	25-40		PIEMA PIBHW	324-340		PVFB VACCC	280-297
PVMT2 IAWIL	25-40		PIEMA PIBHX	324-340		PVFB VACCV	280-297
PVMT9 MYXVL	226-241		PIEMA RINDK	306-383		PVFB VACCC	281-298
			PIEMA SVB	7-84		PVFB VACCV	176-193
			PIEMA SV6CM	7-84		PVFB VACCV	176-193
			PIEMA SV6CP	7-84		PV027 H8V8A	200-226
			PIEMA SV6LN	7-84		PV028 H8V11	173-190
			PVENY OHV11	42-87		PV039 H8V11	646-668
			PVENY EAV	28-41		PV043 H8V11	109-128
			PV022 FOWPV	88-104		PV067 H8V11	171-198
			PV077 CAPVK	88-104		PV072 H8V11	1252-1289
			PV08 VACCC	72-87		PV0F1 BV8	3073-3090
			PV001 H8VEB	188-184		PV0L2 BV8	1084-1111
			PV001 H8V11	208-226		PV0LB H8VE1	736-753
			PV008 H8V11	134-149		PV0LB H8VE4	876-892
			PV010 H8V8A	108-124		PV0LB H8VEB	736-753
			PV011 H8V11	103-119		PV0LB H8VEL	736-753
			PV023 H8V11	270-288		PV0LB ILTV8	897-814
			PV01 8PV1R	70-92		PV0LB ILTV8	807-824
			PV025 H8V11	20-35		PV0LB ILTVT	807-824
			PV088 BPOX2	22-37		PV0LC PRVIF	180-187
			PV038 H8V8A	108-123		PV0LE VZVD	499-486
			PV037 H8V11	284-289		PV0LF SV6	401-418
			PV041 H8V11	244-260		PV0LH HCMVA	385-382
			PV046 H8V11	1244-1260		PV0LH HCMVT	384-381
			PV055 H8V11	22-37		PV0LH H8V11	245-262
			PV056 H8V11	286-283		PV0LH H8V1E	245-262
			PV058 H8V11	101-117		PV0LH H8V11	43-60
			PV066 H8V8A	130-146		PV0LM BUNL7	81-98
			PV068 H8V11	267-282		PV0LM BUNBH	81-98
			PV068 H8V11	382-378		PV0LM PUUMH	712-729
			PV071 H8V8A	89-108		PV0LM PUUM8	712-729
			PV08 BPH2	234-249		PV0LM RVFV	344-361
			PV08 BPF2A	234-249		PV0LM RVFVZ	344-361
			PV08 8PV1R	67-72		PV0LY LA88Q	12-94
			PV0F1 BV8	2210-2226		PV0LY LA88J	12-94
			PV0L3 CV8F	123-139		PV0LY LYCVA	12-94
			PV0L3 CV8L8	123-139		PV0LY LYCVW	12-94
			PV0L3 CV8LY	123-139		PV0LY MOPEI	12-94
			PV0L3 CV8M	123-139		PV0M1 REOVD	280-297
			PV0L3 CV8Q	31-47		PV0M1 REOVL	280-297

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TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,
P5CTLZIP, and P6CTLZIP Motifs

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PVH01 VACCV	83-101	126-144	PVQ12 CVM4	989-1018		PVENV THQCV	366-378	PHEMA P12H	13-34	
PVH1 REOVD	227-246		PVQ12 CVM4S	947-968		PVQ01 VACCV	286-318	PHEMA P12H	13-34	
PVH1 REOVL	227-246		PVQ12 CVM4H	850-877		PVQ01 VACCV	237-267	PHEMA BVB	7-28	379-400
PVHAT H8VA	44-62		PVQ12 CVPF8	84-83	1030-1057	PVQ01 VARV	280-318	PHEMA BVC6M	7-28	379-400
PVHAT NDVA	180-208		PVQ12 CVPPU	84-83	1030-1056	PVQ06 VACCC	31-51	PHEMA BVC6P	7-28	379-400
PVHAT NDVB	180-208		PVQ12 CVPR8	814-833		PVQ06 VARV	26-46	PHEMA BVC6N	7-28	379-400
PVMP CAMVD	183-201		PVQ12 CVPRM	814-833		PVQ06 BPFF1	31-51	PVQ01 HSBVB	189-190	
PVMP CAMVC	183-201		PVQ12 FIPV	1041-1080		PVQ12 H8V11	151-171	PVQ01 H8V11	688-610	
PVMP CAMVE	183-201		PVQ12 IBV8	688-607	771-700	PVQ22 H8V11	300-320	PVQ23 H8V11	214-335	
PVMP CAMVN	183-201		PVQ12 IBV8	688-608	771-700	PVQ22 H8V11	640-668	PVQ37 BPOK2	68-86	
PVMP CAMV9	183-201		PVQ12 IBVD2	688-607	771-700	PVQ51 H8V11	29-49	PVQ43 H8V11	167-178	
PVMP CAMVW	183-201		PVQ12 IBVK	688-608	770-709	PVQ63 H8V11	336-356	PVQ65 H8V11	288-309	
PVMP FMVD	180-188		PVQ12 IBVM	688-608	770-780	PVQ66 H8V11	117-137	PVQ68 H8V11	85-108	
			PVQ18 HCMVA	707-725		PVQ74 H8V8A	124-144	PVQ58 H8V11	1165-1178	
			PVQ18 HCMVT	707-728		PVQ12 IBV8	328-348	PVQ68 H8V8A	206-287	
			PVQ18 H8V8U	117-139		PVQ12 IBV8	327-347	PVQ80 H8V11	30-51	
			PVQ18 ILTV8	260-278		PVQ12 IBVD2	328-348	PVQ83 H8V11	236-269	
			PVQ18 ILTV8	260-285		PVQ12 IBVD3	328-348	PVQF1 IBV8	1856-1877	
			PVQ18 ILTVT	260-285		PVQ12 IBVK	327-347	PVQH3 HCMVA	167-178	
			PVQ18 H8V11	3-84	487-408	PVQ12 IBVM	327-347	PVQ12 CVBF	1269-1280	
			PVQ18 H8V1K	3-84	467-486	PVQ12 IBVU2	310-330	PVQ12 CVBL9	1266-1280	
			PVQ18 H8VBC	476-484		PVQ18 E8V	732-752	PVQ12 CVBLV	1269-1280	
			PVQ18 CHAV	436-455		PVQ18 HCMVA	760-770	PVQ12 CVBM	1269-1280	
			PVQ18 RABVH	372-391		PVQ18 HCMVT	761-771	PVQ12 CVBQ	1269-1280	
			PVQ18 H8V8B	44-63		PVQ18 H8V23	79-89	PVQ12 CVBV	1269-1280	
			PVQ18 V2VD	278-297		PVQ18 H8V2H	79-89	PVQ12 CVM4	1317-1338	
			PVQ18 BUNGE	117-136		PVQ18 H8V2H	65-85	PVQ12 CVM4S	1265-1288	
			PVQ18 PHV	162-171		PVQ18 H8V8U	72-82	PVQ12 CVM4H	1176-1187	
			PVQ18 PTPV	887-1018		PVQ18 H8V82	279-299	PVQ18 H8V11	83-104	
			PVQ18 PUUMH	166-174		PVQ18 H8V8A	83-83	PVQ18 H8V1F	82-103	
			PVQ18 PUUMS	166-174		PVQ18 HCMV8	738-768	PVQ18 H8V1K	82-103	
			PVQ18 RVFV	830-849		PVQ18 P12H4	283-303	PVQ18 H8V1P	83-104	
			PVQ18 RVFV2	830-849		PVQ18 RABVE	454-474	PVQ18 HCMV9	136-160	
			PVQ18 UUK	855-874		PVQ18 RABVH	454-474	PVQ18 CVBF	448-467	
			PVQ18 LYGVW	88-108		PVQ18 RABVP	454-474	PVQ18 CVDO	536-567	
			PVQ18 CMV	1166-1184		PVQ18 RABV8	454-474	PVQ18 MEABE	224-245	
			PVQ18 REOVD	821-840		PVQ18 RABVT	454-474	PVQ18 MEAB1	227-248	
			PVQ18 CVBM	171-180		PVQ18 HCMV8	670-680	PVQ18 MEABY	224-245	
			PVQ18 CVH22	136-166		PVQ18 BUNL7	1328-1348	PVQ18 MUMPM	440-467	
			PVQ18 CVPF8	174-193		PVQ18 BUNH	1328-1346	PVQ18 MUMPR	440-467	
			PVQ18 CVPPU	174-193		PVQ18 BUNVW	988-1018	PVQ18 MUMPS	440-467	
			PVQ18 CVPRM	174-193		PVQ18 HANTH	988-1018	PVQ18 PHODV	368-328	
			PVQ18 CVTKE	171-180		PVQ18 HANTH	1000-1020	PVQ18 PIHC	450-471	
						PVQ18 HANTV	1001-1021	PVQ18 PIH2	450-471	
						PVQ18 HANTV	1001-1021	PVQ18 PIH2	450-471	
						PVQ18 RVFVZ	1166-1176	PVQ18 PIH2	450-471	
						PVQ18 SEOUR	1000-1020	PVQ18 PIH2	450-471	

	PVGLM BEOUS	89B-1018	PVQLF PI3H4	483-474
	PVGLM UIK	926-946	PVQLF RINDK	220-241
	PVGLY LYCVA	12-32	PVQLF RINDL	220-241
	PVGLY LYCVW	12-32	PVQLF SEND6	480-481
	PVGLY PIARV	12-32	PVQLF SENDF	480-481
	PVGNB CPMV	141-161	PVQLF SENDH	480-481
	PVMAT MJUMP9	310-330	PVQLF SENDJ	480-481
	PVMAT NDVA	308-328	PVQLF SENDZ	480-481
	PVMAT NDVB	308-328	PVQLF SV41	453-474
	PVMAT PIZHT	308-328	PVQLF SV6	446-467
	PVMAT PI4HA	312-332	PVQLH HCMVA	881-712
	PVMAT PI4HB	312-332	PVQLH HCMVT	880-711
	PVMAT SV41	308-328	PVQLH HBEZ4	304-326
	PVMAT SV6	308-328	PVQLH HBVE8	287-318
	PVMEI IBV6	74-84	PVQLH HBVA8A	666-679
	PVMEI IBVB	74-84	PVOLI HSV2	2-23
	PVMEI IBVB2	74-84	PVOLI HBV23	2-23
	PVMEI IBVK	74-84	PVQLM BUNDE	187-218
	PVMSA HPBD8	201-221	PVQLM BUNL7	180-211
	PVMSA HPBDB	208-228	PVQLM BUNSH	180-211
	PVMSA HPBHE	203-213	PVQLM BUNYW	183-214
	PVMSA WHV1	207-227	PVQLY LAB8G	232-258
	PVMSA WHV68	212-232	PVQLY LAB9J	238-269
	PVMSA WHV7	212-232	PVQP8 EBV	87-88
	PVMSA WHVB	212-232	PVM01 VACCC	281-302
	PVMSA WHVB8	212-232	PVM01 VACCX	230-261
	PVMSA WHVB8	212-232	PVMAT HR8VA	188-180
	PVMSA WHVWB	83-83	PVMAT RINDK	200-221
			PVMAT TRTV	123-143
			PVMEI CVHOC	64-86
			PVMSA HPBD8	201-222
			PVMSA HPBVO	70-91
			PVMSA HPBV2	244-285
			PVMSA HPBV4	244-285
			PVMSA HPBV8	244-285
			PVMSA HPBVA	233-264
			PVMSA HPBVD	70-91
			PVMSA HPBVI	233-264
			PVMSA HPBVJ	233-264
			PVMSA HPBVL	233-264
			PVMSA HPBVN	70-91
			PVMSA HPBVO	233-264
			PVMSA HPBPV	244-285
			PVMSA HPBVR	244-285
			PVMSA HPBV8	70-91
			PVMSA HPBVW	233-264
			PVMSA HPBVY	233-264

TABLE XII

Search Results Summary for P7CTLZIP,
P8CTLZIP, and P9CTLZIP Motifs

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TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF

PCG CODE	PICTURE	AD Virus (No. Bacteriophage?)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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PROTEIN	FUNCTION	GENE	LOCUS	CHROM.	COORDINATES	REFERENCE
ADAMTS-1	ADAMTS-1	ADAMTS-1	10p11	10	10p11	10p11
ADAMTS-2	ADAMTS-2	ADAMTS-2	10p11	10	10p11	10p11
ADAMTS-3	ADAMTS-3	ADAMTS-3	10p11	10	10p11	10p11
ADAMTS-4	ADAMTS-4	ADAMTS-4	10p11	10	10p11	10p11
ADAMTS-5	ADAMTS-5	ADAMTS-5	10p11	10	10p11	10p11
ADAMTS-6	ADAMTS-6	ADAMTS-6	10p11	10	10p11	10p11
ADAMTS-7	ADAMTS-7	ADAMTS-7	10p11	10	10p11	10p11
ADAMTS-8	ADAMTS-8	ADAMTS-8	10p11	10	10p11	10p11
ADAMTS-9	ADAMTS-9	ADAMTS-9	10p11	10	10p11	10p11
ADAMTS-10	ADAMTS-10	ADAMTS-10	10p11	10	10p11	10p11
ADAMTS-11	ADAMTS-11	ADAMTS-11	10p11	10	10p11	10p11
ADAMTS-12	ADAMTS-12	ADAMTS-12	10p11	10	10p11	10p11
ADAMTS-13	ADAMTS-13	ADAMTS-13	10p11	10	10p11	10p11
ADAMTS-14	ADAMTS-14	ADAMTS-14	10p11	10	10p11	10p11
ADAMTS-15	ADAMTS-15	ADAMTS-15	10p11	10	10p11	10p11
ADAMTS-16	ADAMTS-16	ADAMTS-16	10p11	10	10p11	10p11
ADAMTS-17	ADAMTS-17	ADAMTS-17	10p11	10	10p11	10p11
ADAMTS-18	ADAMTS-18	ADAMTS-18	10p11	10	10p11	10p11
ADAMTS-19	ADAMTS-19	ADAMTS-19	10p11	10	10p11	10p11
ADAMTS-20	ADAMTS-20	ADAMTS-20	10p11	10	10p11	10p11
ADAMTS-21	ADAMTS-21	ADAMTS-21	10p11	10	10p11	10p11
ADAMTS-22	ADAMTS-22	ADAMTS-22	10p11	10	10p11	10p11
ADAMTS-23	ADAMTS-23	ADAMTS-23	10p11	10	10p11	10p11
ADAMTS-24	ADAMTS-24	ADAMTS-24	10p11	10	10p11	10p11
ADAMTS-25	ADAMTS-25	ADAMTS-25	10p11	10	10p11	10p11
ADAMTS-26	ADAMTS-26	ADAMTS-26	10p11	10	10p11	10p11
ADAMTS-27	ADAMTS-27	ADAMTS-27	10p11	10	10p11	10p11
ADAMTS-28	ADAMTS-28	ADAMTS-28	10p11	10	10p11	10p11
ADAMTS-29	ADAMTS-29	ADAMTS-29	10p11	10	10p11	10p11
ADAMTS-30	ADAMTS-30	ADAMTS-30	10p11	10	10p11	10p11
ADAMTS-31	ADAMTS-31	ADAMTS-31	10p11	10	10p11	10p11
ADAMTS-32	ADAMTS-32	ADAMTS-32	10p11	10	10p11	10p11
ADAMTS-33	ADAMTS-33	ADAMTS-33	10p11	10	10p11	10p11
ADAMTS-34	ADAMTS-34	ADAMTS-34	10p11	10	10p11	10p11
ADAMTS-35	ADAMTS-35	ADAMTS-35	10p11	10	10p11	10p11
ADAMTS-36	ADAMTS-36	ADAMTS-36	10p11	10	10p11	10p11
ADAMTS-37	ADAMTS-37	ADAMTS-37	10p11	10	10p11	10p11
ADAMTS-38	ADAMTS-38	ADAMTS-38	10p11	10	10p11	10p11
ADAMTS-39	ADAMTS-39	ADAMTS-39	10p11	10	10p11	10p11
ADAMTS-40	ADAMTS-40	ADAMTS-40	10p11	10	10p11	10p11
ADAMTS-41	ADAMTS-41	ADAMTS-41	10p11	10	10p11	10p11
ADAMTS-42	ADAMTS-42	ADAMTS-42	10p11	10	10p11	10p11
ADAMTS-43	ADAMTS-43	ADAMTS-43	10p11	10	10p11	10p11
ADAMTS-44	ADAMTS-44	ADAMTS-44	10p11	10	10p11	10p11
ADAMTS-45	ADAMTS-45	ADAMTS-45	10p11	10	10p11	10p11
ADAMTS-46	ADAMTS-46	ADAMTS-46	10p11	10	10p11	10p11
ADAMTS-47	ADAMTS-47	ADAMTS-47	10p11	10	10p11	10p11
ADAMTS-48	ADAMTS-48	ADAMTS-48	10p11	10	10p11	10p11
ADAMTS-49	ADAMTS-49	ADAMTS-49	10p11	10	10p11	10p11
ADAMTS-50	ADAMTS-50	ADAMTS-50	10p11	10	10p11	10p11
ADAMTS-51	ADAMTS-51	ADAMTS-51	10p11	10	10p11	10p11
ADAMTS-52	ADAMTS-52	ADAMTS-52	10p11	10	10p11	10p11
ADAMTS-53	ADAMTS-53	ADAMTS-53	10p11	10	10p11	10p11
ADAMTS-54	ADAMTS-54	ADAMTS-54	10p11	10	10p11	10p11
ADAMTS-55	ADAMTS-55	ADAMTS-55	10p11	10	10p11	10p11
ADAMTS-56	ADAMTS-56	ADAMTS-56	10p11	10	10p11	10p11
ADAMTS-57	ADAMTS-57	ADAMTS-57	10p11	10	10p11	10p11
ADAMTS-58	ADAMTS-58	ADAMTS-58	10p11	10	10p11	10p11
ADAMTS-59	ADAMTS-59	ADAMTS-59	10p11	10	10p11	10p11
ADAMTS-60	ADAMTS-60	ADAMTS-60	10p11	10	10p11	10p11
ADAMTS-61	ADAMTS-61	ADAMTS-61	10p11	10	10p11	10p11
ADAMTS-62	ADAMTS-62	ADAMTS-62	10p11	10	10p11	10p11
ADAMTS-63	ADAMTS-63	ADAMTS-63	10p11	10	10p11	10p11
ADAMTS-64	ADAMTS-64	ADAMTS-64	10p11	10	10p11	10p11
ADAMTS-65	ADAMTS-65	ADAMTS-65	10p11	10	10p11	10p11
ADAMTS-66	ADAMTS-66	ADAMTS-66	10p11	10	10p11	10p11
ADAMTS-67	ADAMTS-67	ADAMTS-67	10p11	10	10p11	10p11
ADAMTS-68	ADAMTS-68	ADAMTS-68	10p11	10	10p11	10p11
ADAMTS-69	ADAMTS-69	ADAMTS-69	10p11	10	10p11	10p11
ADAMTS-70	ADAMTS-70	ADAMTS-70	10p11	10	10p11	10p11
ADAMTS-71	ADAMTS-71	ADAMTS-71	10p11	10	10p11	10p11
ADAMTS-72	ADAMTS-72	ADAMTS-72	10p11	10	10p11	10p11
ADAMTS-73	ADAMTS-73	ADAMTS-73	10p11	10	10p11	10p11
ADAMTS-74	ADAMTS-74	ADAMTS-74	10p11	10	10p11	10p11
ADAMTS-75	ADAMTS-75	ADAMTS-75	10p11	10	10p11	10p11
ADAMTS-76	ADAMTS-76	ADAMTS-76	10p11	10	10p11	10p11
ADAMTS-77	ADAMTS-77	ADAMTS-77	10p11	10	10p11	10p11
ADAMTS-78	ADAMTS-78	ADAMTS-78	10p11	10	10p11	10p11
ADAMTS-79	ADAMTS-79	ADAMTS-79	10p11	10	10p11	10p11
ADAMTS-80	ADAMTS-80	ADAMTS-80	10p11	10	10p11	10p11
ADAMTS-81	ADAMTS-81	ADAMTS-81	10p11	10	10p11	10p11
ADAMTS-82	ADAMTS-82	ADAMTS-82	10p11	10	10p11	10p11
ADAMTS-83	ADAMTS-83	ADAMTS-83	10p11	10	10p11	10p11
ADAMTS-84	ADAMTS-84	ADAMTS-84	10p11	10	10p11	10p11
ADAMTS-85	ADAMTS-85	ADAMTS-85	10p11	10	10p11	10p11
ADAMTS-86	ADAMTS-86	ADAMTS-86	10p11	10	10p11	10p11
ADAMTS-87	ADAMTS-87	ADAMTS-87	10p11	10	10p11	10p11
ADAMTS-88	ADAMTS-88	ADAMTS-88	10p11	10	10p11	10p11
ADAMTS-89	ADAMTS-89	ADAMTS-89	10p11	10	10p11	10p11
ADAMTS-90	ADAMTS-90	ADAMTS-90	10p11	10	10p11	10p11
ADAMTS-91	ADAMTS-91	ADAMTS-91	10p11	10	10p11	10p11
ADAMTS-92	ADAMTS-92	ADAMTS-92	10p11	10	10p11	10p11
ADAMTS-93	ADAMTS-93	ADAMTS-93	10p11	10	10p11	10p11
ADAMTS-94	ADAMTS-94	ADAMTS-94	10p11	10	10p11	10p11
ADAMTS-95	ADAMTS-95	ADAMTS-95	10p11	10	10p11	10p11
ADAMTS-96	ADAMTS-96	ADAMTS-96	10p11	10	10p11	10p11
ADAMTS-97	ADAMTS-97	ADAMTS-97	10p11	10	10p11	10p11
ADAMTS-98	ADAMTS-98	ADAMTS-98	10p11	10	10p11	10p11
ADAMTS-99	ADAMTS-99	ADAMTS-99	10p11	10	10p11	10p11
ADAMTS-100	ADAMTS-100	ADAMTS-100	10p11	10	10p11	10p11
ADAMTS-101	ADAMTS-101	ADAMTS-101	10p11	10	10p11	10p11
ADAMTS-102	ADAMTS-102	ADAMTS-102	10p11	10	10p11	10p11
ADAMTS-103	ADAMTS-103	ADAMTS-103	10p11	10	10p11	10p11
ADAMTS-104	ADAMTS-104	ADAMTS-104	10p11	10	10p11	10p11
ADAMTS-105	ADAMTS-105	ADAMTS-105	10p11	10	10p11	10p11
ADAMTS-106	ADAMTS-106	ADAMTS-106	10p11	10	10p11	10p11
ADAMTS-107	ADAMTS-107	ADAMTS-107	10p11	10	10p11	10p11
ADAMTS-108	ADAMTS-108	ADAMTS-108	10p11	10	10p11	10p11
ADAMTS-109	ADAMTS-109	ADAMTS-109	10p11	10	10p11	10p11
ADAMTS-110	ADAMTS-110	ADAMTS-110	10p11	10	10p11	10p11
ADAMTS-111	ADAMTS-111	ADAMTS-111	10p11	10	10p11	10p11
ADAMTS-112	ADAMTS-112	ADAMTS-112	10p11	10	10p11	10p11
ADAMTS-113	ADAMTS-113	ADAMTS-113	10p11	10	10p11	10p11
ADAMTS-114	ADAMTS-114	ADAMTS-114	10p11	10	10p11	10p11
ADAMTS-115	ADAMTS-115	ADAMTS-115	10p11	10	10p11	10p11
ADAMTS-116	ADAMTS-116	ADAMTS-116	10p11	10	10p11	10p11
ADAMTS-117	ADAMTS-117	ADAMTS-117	10p11	10	10p11	10p11
ADAMTS-118	ADAMTS-118	ADAMTS-118	10p11	10	10p11	10p11
ADAMTS-119	ADAMTS-119	ADAMTS-119	10p11	10	10p11	10p11
ADAMTS-120	ADAMTS-120	ADAMTS-120	10p11	10	10p11	10p11
ADAMTS-121	ADAMTS-121	ADAMTS-121	10p11	10	10p11	10p11
ADAMTS-122	ADAMTS-122	ADAMTS-122	10p11	10	10p11	10p11
ADAMTS-123	ADAMTS-123	ADAMTS-123	10p11	10	10p11	10p11
ADAMTS-124	ADAMTS-124	ADAMTS-124	10p11	10	10p11	10p11
ADAMTS-125	ADAMTS-125	ADAMTS-125	10p11	10	10p11	10p11
ADAMTS-126	ADAMTS-126	ADAMTS-126	10p11	10	10p11	10p11
ADAMTS-127	ADAMTS-127	ADAMTS-127	10p11	10	10p11	10p11
ADAMTS-128	ADAMTS-128	ADAMTS-128	10p11	10	10p11	10p11
ADAMTS-129	ADAMTS-129	ADAMTS-129	10p11	10	10p11	10p11
ADAMTS-130	ADAMTS-130	ADAMTS-130	10p11	10	10p11	10p11
ADAMTS-131	ADAMTS-131	ADAMTS-131	10p11	10	10p11	10p11
ADAMTS-132	ADAMTS-132	ADAMTS-132	10p11	10	10p11	10p11
ADAMTS-133	ADAMTS-133	ADAMTS-133	10p11	10	10p11	10p11
ADAMTS-134	ADAMTS-134	ADAMTS-134	10p11	10	10p11	10p11
ADAMTS-135	ADAMTS-135	ADAMTS-135	10p11	10	10p11	10p11
ADAMTS-136	ADAMTS-136	ADAMTS-136	10p11	10	10p11	10p11
ADAMTS-137	ADAMTS-137	ADAMTS-137	10p11	10	10p11	10p11
ADAMTS-138	ADAMTS-138	ADAMTS-138	10p11	10	10p11	10p11
ADAMTS-139	ADAMTS-139	ADAMTS-139	10p11	10	10p11	10p11
ADAMTS-140	ADAMTS-140	ADAMTS-140	10p11	10	10p11	10p11
ADAMTS-141	ADAMTS-141	ADAMTS-141	10p11	10	10p11	10p11
ADAMTS-142	ADAMTS-142	ADAMTS-142	10p11	10	10p11	10p11
ADAMTS-143	ADAMTS-143	ADAMTS-143	10p11	10	10p11	10p11
ADAMTS-144	ADAMTS-144	ADAMTS-144	10p11	10	10p11	10p11
ADAMTS-145	ADAMTS-145	ADAMTS-145	10p11	10	10p11	10p11
ADAMTS-146	ADAMTS-146	ADAMTS-146	10p11	10	10p11	10p11
ADAMTS-147	ADAMTS-147	ADAMTS-147	10p11	10	10p11	10p11
ADAMTS-148	ADAMTS-148	ADAMTS-148	10p11	10	10p11	10p11
ADAMTS-149	ADAMTS-149	ADAMTS-149	10p11	10	10p11	10p11
ADAMTS-150	ADAMTS-150	ADAMTS-150	10p11	10	10p11	10p11
ADAMTS-151	ADAMTS-151	ADAMTS-151	10p11	10	10p11	10p11
ADAMTS-152	ADAMTS-152	ADAMTS-152	10p11	10	10p11	10p11
ADAMTS-153	ADAMTS-153	ADAMTS-153	10p11	10	10p11	10p11
ADAMTS-154	ADAMTS-154	ADAMTS-154	10p11	10	10p11	10p11
ADAMTS-155	ADAMTS-155	ADAMTS-155	10p11	10	10p11	10p11
ADAMTS-156	ADAMTS-156	ADAMTS-156	10p11	10	10p11	10p11
ADAMTS-157	ADAMTS-157	ADAMTS-157	10p11	10	10p11	10p11
ADAMTS-158	ADAMTS-158	ADAMTS-158	10p11	10	10p11	10p11
ADAMTS-159	ADAMTS-159	ADAMTS-159	10p11	10	10p11	10p11
ADAMTS-160	ADAMTS-160	ADAMTS-160	10p11	10	10p11	10p11
ADAMTS-161	ADAMTS-161	ADAMTS-161	10p11	10	10p11	10p11
ADAMTS-162	ADAMTS-162	ADAMTS-162	10p11	10	10p11	10p11
ADAMTS-163	ADAMTS-163	ADAMTS-163	10p11	10	10p11	10p11
ADAMTS-164	ADAMTS-164	ADAMTS-164	10p11	10	10p11	10p11
ADAMTS-165	ADAMTS-165					

COLLAGE	PROJECT/ZIP	VIRUS	ALL VIRUS (No. Battering Charge?)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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GENE	PROTEIN	PICTURE	AR Virus (No. Bacteriophage)	ARV1	ARV2	ARV3	ARV4	ARV5	ARV6	ARV7	ARV8	ARV9	ARV10	ARV11	ARV12	ARV13	ARV14	ARV15	ARV16	ARV17	ARV18	ARV19	ARV20	ARV21	ARV22	ARV23	ARV24	ARV25	ARV26	ARV27	ARV28	ARV29	ARV30	ARV31	ARV32	ARV33	ARV34	ARV35	ARV36	ARV37	ARV38	ARV39	ARV40	ARV41	ARV42	ARV43	ARV44	ARV45	ARV46	ARV47	ARV48	ARV49	ARV50	ARV51	ARV52	ARV53	ARV54	ARV55	ARV56	ARV57	ARV58	ARV59	ARV60	ARV61	ARV62	ARV63	ARV64	ARV65	ARV66	ARV67	ARV68	ARV69	ARV70	ARV71	ARV72	ARV73	ARV74	ARV75	ARV76	ARV77	ARV78	ARV79	ARV80	ARV81	ARV82	ARV83	ARV84	ARV85	ARV86	ARV87	ARV88	ARV89	ARV90	ARV91	ARV92	ARV93	ARV94	ARV95	ARV96	ARV97	ARV98	ARV99	ARV100	ARV101	ARV102	ARV103	ARV104	ARV105	ARV106	ARV107	ARV108	ARV109	ARV110	ARV111	ARV112	ARV113	ARV114	ARV115	ARV116	ARV117	ARV118	ARV119	ARV120	ARV121	ARV122	ARV123	ARV124	ARV125	ARV126	ARV127	ARV128	ARV129	ARV130	ARV131	ARV132	ARV133	ARV134	ARV135	ARV136	ARV137	ARV138	ARV139	ARV140	ARV141	ARV142	ARV143	ARV144	ARV145	ARV146	ARV147	ARV148	ARV149	ARV150	ARV151	ARV152	ARV153	ARV154	ARV155	ARV156	ARV157	ARV158	ARV159	ARV160	ARV161	ARV162	ARV163	ARV164	ARV165	ARV166	ARV167	ARV168	ARV169	ARV170	ARV171	ARV172	ARV173	ARV174	ARV175	ARV176	ARV177	ARV178	ARV179	ARV180	ARV181	ARV182	ARV183	ARV184	ARV185	ARV186	ARV187	ARV188	ARV189	ARV190	ARV191	ARV192	ARV193	ARV194	ARV195	ARV196	ARV197	ARV198	ARV199	ARV200	ARV201	ARV202	ARV203	ARV204	ARV205	ARV206	ARV207	ARV208	ARV209	ARV210	ARV211	ARV212	ARV213	ARV214	ARV215	ARV216	ARV217	ARV218	ARV219	ARV220	ARV221	ARV222	ARV223	ARV224	ARV225	ARV226	ARV227	ARV228	ARV229	ARV230	ARV231	ARV232	ARV233	ARV234	ARV235	ARV236	ARV237	ARV238	ARV239	ARV240	ARV241	ARV242	ARV243	ARV244	ARV245	ARV246	ARV247	ARV248	ARV249	ARV250	ARV251	ARV252	ARV253	ARV254	ARV255	ARV256	ARV257	ARV258	ARV259	ARV260	ARV261	ARV262	ARV263	ARV264	ARV265	ARV266	ARV267	ARV268	ARV269	ARV270	ARV271	ARV272	ARV273	ARV274	ARV275	ARV276	ARV277	ARV278	ARV279	ARV280	ARV281	ARV282	ARV283	ARV284	ARV285	ARV286	ARV287	ARV288	ARV289	ARV290	ARV291	ARV292	ARV293	ARV294	ARV295	ARV296	ARV297	ARV298	ARV299	ARV300	ARV301	ARV302	ARV303	ARV304	ARV305	ARV306	ARV307	ARV308	ARV309	ARV310	ARV311	ARV312	ARV313	ARV314	ARV315	ARV316	ARV317	ARV318	ARV319	ARV320	ARV321	ARV322	ARV323	ARV324	ARV325	ARV326	ARV327	ARV328	ARV329	ARV330	ARV331	ARV332	ARV333	ARV334	ARV335	ARV336	ARV337	ARV338	ARV339	ARV340	ARV341	ARV342	ARV343	ARV344	ARV345	ARV346	ARV347	ARV348	ARV349	ARV350	ARV351	ARV352	ARV353	ARV354	ARV355	ARV356	ARV357	ARV358	ARV359	ARV360	ARV361	ARV362	ARV363	ARV364	ARV365	ARV366	ARV367	ARV368	ARV369	ARV370	ARV371	ARV372	ARV373	ARV374	ARV375	ARV376	ARV377	ARV378	ARV379	ARV380	ARV381	ARV382	ARV383	ARV384	ARV385	ARV386	ARV387	ARV388	ARV389	ARV390	ARV391	ARV392	ARV393	ARV394	ARV395	ARV396	ARV397	ARV398	ARV399	ARV400	ARV401	ARV402	ARV403	ARV404	ARV405	ARV406	ARV407	ARV408	ARV409	ARV410	ARV411	ARV412	ARV413	ARV414	ARV415	ARV416	ARV417	ARV418	ARV419	ARV420	ARV421	ARV422	ARV423	ARV424	ARV425	ARV426	ARV427	ARV428	ARV429	ARV430	ARV431	ARV432	ARV433	ARV434	ARV435	ARV436	ARV437	ARV438	ARV439	ARV440	ARV441	ARV442	ARV443	ARV444	ARV445	ARV446	ARV447	ARV448	ARV449	ARV450	ARV451	ARV452	ARV453	ARV454	ARV455	ARV456	ARV457	ARV458	ARV459	ARV460	ARV461	ARV462	ARV463	ARV464	ARV465	ARV466	ARV467	ARV468	ARV469	ARV470	ARV471	ARV472	ARV473	ARV474	ARV475	ARV476	ARV477	ARV478	ARV479	ARV480	ARV481	ARV482	ARV483	ARV484	ARV485	ARV486	ARV487	ARV488	ARV489	ARV490	ARV491	ARV492	ARV493	ARV494	ARV495	ARV496	ARV497	ARV498	ARV499	ARV500	ARV501	ARV502	ARV503	ARV504	ARV505	ARV506	ARV507	ARV508	ARV509	ARV510	ARV511	ARV512	ARV513	ARV514	ARV515	ARV516	ARV517	ARV518	ARV519	ARV520	ARV521	ARV522	ARV523	ARV524	ARV525	ARV526	ARV527	ARV528	ARV529	ARV530	ARV531	ARV532	ARV533	ARV534	ARV535	ARV536	ARV537	ARV538	ARV539	ARV540	ARV541	ARV542	ARV543	ARV544	ARV545	ARV546	ARV547	ARV548	ARV549	ARV550	ARV551	ARV552	ARV553	ARV554	ARV555	ARV556	ARV557	ARV558	ARV559	ARV560	ARV561	ARV562	ARV563	ARV564	ARV565	ARV566	ARV567	ARV568	ARV569	ARV570	ARV571	ARV572	ARV573	ARV574	ARV575	ARV576	ARV577	ARV578	ARV579	ARV580	ARV581	ARV582	ARV583	ARV584	ARV585	ARV586	ARV587	ARV588	ARV589	ARV590	ARV591	ARV592	ARV593	ARV594	ARV595	ARV596	ARV597	ARV598	ARV599	ARV600	ARV601	ARV602	ARV603	ARV604	ARV605	ARV606	ARV607	ARV608	ARV609	ARV610	ARV611	ARV612	ARV613	ARV614	ARV615	ARV616	ARV617	ARV618	ARV619	ARV620	ARV621	ARV622	ARV623	ARV624	ARV625	ARV626	ARV627	ARV628	ARV629	ARV630	ARV631	ARV632	ARV633	ARV634	ARV635	ARV636	ARV637	ARV638	ARV639	ARV640	ARV641	ARV642	ARV643	ARV644	ARV645	ARV646	ARV647	ARV648	ARV649	ARV650	ARV651	ARV652	ARV653	ARV654	ARV655	ARV656	ARV657	ARV658	ARV659	ARV660	ARV661	ARV662	ARV663	ARV664	ARV665	ARV666	ARV667	ARV668	ARV669	ARV670	ARV671	ARV672	ARV673	ARV674	ARV675	ARV676	ARV677	ARV678	ARV679	ARV680	ARV681	ARV682	ARV683	ARV684	ARV685	ARV686	ARV687	ARV688	ARV689	ARV690	ARV691	ARV692	ARV693	ARV694	ARV695	ARV696	ARV697	ARV698	ARV699	ARV700	ARV701	ARV702	ARV703	ARV704	ARV705	ARV706	ARV707	ARV708	ARV709	ARV710	ARV711	ARV712	ARV713	ARV714	ARV715	ARV716	ARV717	ARV718	ARV719	ARV720	ARV721	ARV722	ARV723	ARV724	ARV725	ARV726	ARV727	ARV7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PRIORITY		VIRUS		AREA 1		AREA 2		AREA 3		AREA 4		AREA 5		AREA 6		AREA 7		AREA 8		AREA 9		AREA 10		AREA 11		AREA 12		AREA 13		AREA 14		AREA 15		AREA 16		AREA 17		AREA 18		AREA 19		AREA 20		AREA 21		AREA 22		AREA 23		AREA 24		AREA 25		AREA 26		AREA 27		AREA 28		AREA 29		AREA 30		AREA 31		AREA 32		AREA 33		AREA 34		AREA 35		AREA 36		AREA 37		AREA 38		AREA 39		AREA 40		AREA 41		AREA 42		AREA 43		AREA 44		AREA 45		AREA 46		AREA 47		AREA 48		AREA 49		AREA 50		AREA 51		AREA 52		AREA 53		AREA 54		AREA 55		AREA 56		AREA 57		AREA 58		AREA 59		AREA 60		AREA 61		AREA 62		AREA 63		AREA 64		AREA 65		AREA 66		AREA 67		AREA 68		AREA 69		AREA 70		AREA 71		AREA 72		AREA 73		AREA 74		AREA 75		AREA 76		AREA 77		AREA 78		AREA 79		AREA 80		AREA 81		AREA 82		AREA 83		AREA 84		AREA 85		AREA 86		AREA 87		AREA 88		AREA 89		AREA 90		AREA 91		AREA 92		AREA 93		AREA 94		AREA 95		AREA 96		AREA 97		AREA 98		AREA 99		AREA 100		AREA 101		AREA 102		AREA 103		AREA 104		AREA 105		AREA 106		AREA 107		AREA 108		AREA 109		AREA 110		AREA 111		AREA 112		AREA 113		AREA 114		AREA 115		AREA 116		AREA 117		AREA 118		AREA 119		AREA 120		AREA 121		AREA 122		AREA 123		AREA 124		AREA 125		AREA 126		AREA 127		AREA 128		AREA 129		AREA 130		AREA 131		AREA 132		AREA 133		AREA 134		AREA 135		AREA 136		AREA 137		AREA 138		AREA 139		AREA 140		AREA 141		AREA 142		AREA 143		AREA 144		AREA 145		AREA 146		AREA 147		AREA 148		AREA 149		AREA 150		AREA 151		AREA 152		AREA 153		AREA 154		AREA 155		AREA 156		AREA 157		AREA 158		AREA 159		AREA 160		AREA 161		AREA 162		AREA 163		AREA 164		AREA 165		AREA 166		AREA 167		AREA 168		AREA 169		AREA 170		AREA 171		AREA 172		AREA 173		AREA 174		AREA 175		AREA 176		AREA 177		AREA 178		AREA 179		AREA 180		AREA 181		AREA 182		AREA 183		AREA 184		AREA 185		AREA 186		AREA 187		AREA 188		AREA 189		AREA 190		AREA 191		AREA 192		AREA 193		AREA 194		AREA 195		AREA 196		AREA 197		AREA 198		AREA 199		AREA 200		AREA 201		AREA 202		AREA 203		AREA 204		AREA 205		AREA 206		AREA 207		AREA 208		AREA 209		AREA 210		AREA 211		AREA 212		AREA 213		AREA 214		AREA 215		AREA 216		AREA 217		AREA 218		AREA 219		AREA 220		AREA 221		AREA 222		AREA 223		AREA 224		AREA 225		AREA 226		AREA 227		AREA 228		AREA 229		AREA 230		AREA 231		AREA 232		AREA 233		AREA 234		AREA 235		AREA 236		AREA 237		AREA 238		AREA 239		AREA 240		AREA 241		AREA 242		AREA 243		AREA 244		AREA 245		AREA 246		AREA 247		AREA 248		AREA 249		AREA 250		AREA 251		AREA 252		AREA 253		AREA 254		AREA 255		AREA 256		AREA 257		AREA 258		AREA 259		AREA 260		AREA 261		AREA 262		AREA 263		AREA 264		AREA 265		AREA 266		AREA 267		AREA 268		AREA 269		AREA 270		AREA 271		AREA 272		AREA 273		AREA 274		AREA 275		AREA 276		AREA 277		AREA 278		AREA 279		AREA 280		AREA 281		AREA 282		AREA 283		AREA 284		AREA 285		AREA 286		AREA 287		AREA 288		AREA 289		AREA 290		AREA 291		AREA 292		AREA 293		AREA 294		AREA 295		AREA 296		AREA 297		AREA 298</	
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PROTEIN		PIST/ZIP	All Viruses (No Bacteriophages)		AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
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PICT31P	PCGZFE	FILE NAME	PROTIN	ALL Viruses (No. Nucleotidephages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	
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GENE	PROTEIN	PICTURE	All Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PROTEIN	FUNCTION	ALL Viruses (No. Nucleotide positions)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA
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TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF

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FUNCTION		PROTEIN		AU Virus (as best as possible)		AREA-1	AREA-2	AREA-3	AREA-4	AREA-5	AREA-6	AREA-7	AREA-8	AREA-9	AREA-10	AREA-11	AREA-12	AREA-13	AREA-14	AREA-15	AREA-16	AREA-17	AREA-18	AREA-19	AREA-20	AREA-21	AREA-22	AREA-23	AREA-24	AREA-25	AREA-26	AREA-27	AREA-28	AREA-29	AREA-30	AREA-31	AREA-32	AREA-33	AREA-34	AREA-35	AREA-36	AREA-37	AREA-38	AREA-39	AREA-40	AREA-41	AREA-42	AREA-43	AREA-44	AREA-45	AREA-46	AREA-47	AREA-48	AREA-49	AREA-50	AREA-51	AREA-52	AREA-53	AREA-54	AREA-55	AREA-56	AREA-57	AREA-58	AREA-59	AREA-60	AREA-61	AREA-62	AREA-63	AREA-64	AREA-65	AREA-66	AREA-67	AREA-68	AREA-69	AREA-70	AREA-71	AREA-72	AREA-73	AREA-74	AREA-75	AREA-76	AREA-77	AREA-78	AREA-79	AREA-80	AREA-81	AREA-82	AREA-83	AREA-84	AREA-85	AREA-86	AREA-87	AREA-88	AREA-89	AREA-90	AREA-91	AREA-92	AREA-93	AREA-94	AREA-95	AREA-96	AREA-97	AREA-98	AREA-99	AREA-100	AREA-101	AREA-102	AREA-103	AREA-104	AREA-105	AREA-106	AREA-107	AREA-108	AREA-109	AREA-110	AREA-111	AREA-112	AREA-113	AREA-114	AREA-115	AREA-116	AREA-117	AREA-118	AREA-119	AREA-120	AREA-121	AREA-122	AREA-123	AREA-124	AREA-125	AREA-126	AREA-127	AREA-128	AREA-129	AREA-130	AREA-131	AREA-132	AREA-133	AREA-134	AREA-135	AREA-136	AREA-137	AREA-138	AREA-139	AREA-140	AREA-141	AREA-142	AREA-143	AREA-144	AREA-145	AREA-146	AREA-147	AREA-148	AREA-149	AREA-150	AREA-151	AREA-152	AREA-153	AREA-154	AREA-155	AREA-156	AREA-157	AREA-158	AREA-159	AREA-160	AREA-161	AREA-162	AREA-163	AREA-164	AREA-165	AREA-166	AREA-167	AREA-168	AREA-169	AREA-170	AREA-171	AREA-172	AREA-173	AREA-174	AREA-175	AREA-176	AREA-177	AREA-178	AREA-179	AREA-180	AREA-181	AREA-182	AREA-183	AREA-184	AREA-185	AREA-186	AREA-187	AREA-188	AREA-189	AREA-190	AREA-191	AREA-192	AREA-193	AREA-194	AREA-195	AREA-196	AREA-197	AREA-198	AREA-199	AREA-200	AREA-201	AREA-202	AREA-203	AREA-204	AREA-205	AREA-206	AREA-207	AREA-208	AREA-209	AREA-210	AREA-211	AREA-212	AREA-213	AREA-214	AREA-215	AREA-216	AREA-217	AREA-218	AREA-219	AREA-220	AREA-221	AREA-222	AREA-223	AREA-224	AREA-225	AREA-226	AREA-227	AREA-228	AREA-229	AREA-230	AREA-231	AREA-232	AREA-233	AREA-234	AREA-235	AREA-236	AREA-237	AREA-238	AREA-239	AREA-240	AREA-241	AREA-242	AREA-243	AREA-244	AREA-245	AREA-246	AREA-247	AREA-248	AREA-249	AREA-250	AREA-251	AREA-252	AREA-253	AREA-254	AREA-255	AREA-256	AREA-257	AREA-258	AREA-259	AREA-260	AREA-261	AREA-262	AREA-263	AREA-264	AREA-265	AREA-266	AREA-267	AREA-268	AREA-269	AREA-270	AREA-271	AREA-272	AREA-273	AREA-274	AREA-275	AREA-276	AREA-277	AREA-278	AREA-279	AREA-280	AREA-281	AREA-282	AREA-283	AREA-284	AREA-285	AREA-286	AREA-287	AREA-288	AREA-289	AREA-290	AREA-291	AREA-292	AREA-293	AREA-294	AREA-295	AREA-296	AREA-297	AREA-298	AREA-299	AREA-300	AREA-301	AREA-302	AREA-303	AREA-304	AREA-305	AREA-306	AREA-307	AREA-308	AREA-309	AREA-310	AREA-311	AREA-312	AREA-313	AREA-314	AREA-315	AREA-316	AREA-317	AREA-318	AREA-319	AREA-320	AREA-321	AREA-322	AREA-323	AREA-324	AREA-325	AREA-326	AREA-327	AREA-328	AREA-329	AREA-330	AREA-331	AREA-332	AREA-333	AREA-334	AREA-335	AREA-336	AREA-337	AREA-338	AREA-339	AREA-340	AREA-341	AREA-342	AREA-343	AREA-344	AREA-345	AREA-346	AREA-347	AREA-348	AREA-349	AREA-350	AREA-351	AREA-352	AREA-353	AREA-354	AREA-355	AREA-356	AREA-357	AREA-358	AREA-359	AREA-360	AREA-361	AREA-362	AREA-363	AREA-364	AREA-365	AREA-366	AREA-367	AREA-368	AREA-369	AREA-370	AREA-371	AREA-372	AREA-373	AREA-374	AREA-375	AREA-376	AREA-377	AREA-378	AREA-379	AREA-380	AREA-381	AREA-382	AREA-383	AREA-384	AREA-385	AREA-386	AREA-387	AREA-388	AREA-389	AREA-390	AREA-391	AREA-392	AREA-393	AREA-394	AREA-395	AREA-396	AREA-397	AREA-398	AREA-399	AREA-400	AREA-401	AREA-402	AREA-403	AREA-404	AREA-405	AREA-406	AREA-407	AREA-408	AREA-409	AREA-410	AREA-411	AREA-412	AREA-413	AREA-414	AREA-415	AREA-416	AREA-417	AREA-418	AREA-419	AREA-420	AREA-421	AREA-422	AREA-423	AREA-424	AREA-425	AREA-426	AREA-427	AREA-428	AREA-429	AREA-430	AREA-431	AREA-432	AREA-433	AREA-434	AREA-435	AREA-436	AREA-437	AREA-438	AREA-439	AREA-440	AREA-441	AREA-442	AREA-443	AREA-444	AREA-445	AREA-446	AREA-447	AREA-448	AREA-449	AREA-450	AREA-451	AREA-452	AREA-453	AREA-454	AREA-455	AREA-456	AREA-457	AREA-458	AREA-459	AREA-460	AREA-461	AREA-462	AREA-463	AREA-464	AREA-465	AREA-466	AREA-467	AREA-468	AREA-469	AREA-470	AREA-471	AREA-472	AREA-473	AREA-474	AREA-475	AREA-476	AREA-477	AREA-478	AREA-479	AREA-480	AREA-481	AREA-482	AREA-483	AREA-484	AREA-485	AREA-486	AREA-487	AREA-488	AREA-489	AREA-490	AREA-491	AREA-492	AREA-493	AREA-494	AREA-495	AREA-496	AREA-497	AREA-498	AREA-499	AREA-500	AREA-501	AREA-502	AREA-503	AREA-504	AREA-505	AREA-506	AREA-507	AREA-508	AREA-509	AREA-510	AREA-511	AREA-512	AREA-513	AREA-514	AREA-515	AREA-516	AREA-517	AREA-518	AREA-519	AREA-520	AREA-521	AREA-522	AREA-523	AREA-524	AREA-525	AREA-526	AREA-527	AREA-528	AREA-529	AREA-530	AREA-531	AREA-532	AREA-533	AREA-534	AREA-535	AREA-536	AREA-537	AREA-538	AREA-539	AREA-540	AREA-541	AREA-542	AREA-543	AREA-544	AREA-545	AREA-546	AREA-547	AREA-548	AREA-549	AREA-550	AREA-551	AREA-552	AREA-553	AREA-554	AREA-555	AREA-556	AREA-557	AREA-558	AREA-559	AREA-560	AREA-561	AREA-562	AREA-563	AREA-564	AREA-565	AREA-566	AREA-567	AREA-568	AREA-569	AREA-570	AREA-571	AREA-572	AREA-573	AREA-574	AREA-575	AREA-576	AREA-577	AREA-578	AREA-579	AREA-580	AREA-581	AREA-582	AREA-583	AREA-584	AREA-585	AREA-586	AREA-587	AREA-588	AREA-589	AREA-590	AREA-591	AREA-592	AREA-593	AREA-594	AREA-595	AREA-596	AREA-597	AREA-598	AREA-599	AREA-600	AREA-601	AREA-602	AREA-603	AREA-604	AREA-605	AREA-606	AREA-607	AREA-608	AREA-609	AREA-610	AREA-611	AREA-612	AREA-613	AREA-614	AREA-615	AREA-616	AREA-617	AREA-618	AREA-619	AREA-620	AREA-621	AREA-622	AREA-623	AREA-624	AREA-625	AREA-626	AREA-627	AREA-628	AREA-629	AREA-630	AREA-631	AREA-632	AREA-633	AREA-634	AREA-635	AREA-636	AREA-637	AREA-638	AREA-639	AREA-640	AREA-641	AREA-642	AREA-643	AREA-644	AREA-645	AREA-646	AREA-647	AREA-648	AREA-649	AREA-650	AREA-651	AREA-652	AREA-653	AREA-654	AREA-655	AREA-656	AREA-657	AREA-658	AREA-659	AREA-660	AREA-661	AREA-662	AREA-663	AREA-664	AREA-665	AREA-666	AREA-667	AREA-668	AREA-669	AREA-670	AREA-671	AREA-672	AREA-673	AREA-674	AREA-675	AREA-676	AREA-677	AREA-678	AREA-679	AREA-680	AREA-681	AREA-682	AREA-683	AREA-684	AREA-685	AREA-686	AREA-687	AREA-688	AREA-689	AREA-690	AREA-691	AREA-692	AREA-693	AREA-694	AREA-695	AREA-696	AREA-697	AREA-698	AREA-699	AREA-700	AREA-701	AREA-702	AREA-703	AREA-704	AREA-705	AREA-706	AREA-707	AREA-708	AREA-709	AREA-710	AREA-711	AREA-712	AREA-713	AREA-714	AREA-715	AREA-716	AREA-717	AREA-718	AREA-719	AREA-720	AREA-721	AREA-722	AREA-723	AREA-724	AREA-725	AREA-726	AREA-727	AREA-728	AREA-729	AREA-730	AREA-731	AREA-732	AREA-733	AREA-734	AREA-735	AREA-736	AREA-737	AREA-738	AREA-739	AREA-740	AREA-741	AREA-742	AREA-743	AREA-744	AREA-745	AREA-746	AREA-747	AREA-748	AREA-749	AREA-750	AREA-751	AREA-752	AREA-753	AREA-754	AREA-755	AREA-756	AREA-757	AREA-758	AREA-759	AREA-760	AREA-761	AREA-762	AREA-763	AREA-764	AREA-765	AREA-766	AREA-767	AREA-768	AREA-769	AREA-770	AREA-771	AREA-772	AREA-773	AREA-774	AREA-775	AREA-776	AREA-777	AREA-778	AREA-779	AREA-780	AREA-781	AREA-782	AREA-783	AREA-784	AREA-785	AREA-786	AREA-787	AREA-788	AREA-789	AREA-790	AREA-791	AREA-792	AREA-793	AREA-794	AREA-795	AREA-796	AREA-797	AREA-798	AREA-799	AREA-800	AREA-801	AREA-802	AREA-803	AREA-804	AREA-805	AREA-806	AREA-807	AREA-808	AREA-809	AREA-810	AREA-811	AREA-812	AREA-813	AREA-814	AREA-815	AREA-816	AREA-817	AREA-818	AREA-819	AREA-820	AREA-821	AREA-822	AREA-823	AREA-824	AREA-825	AREA-826	AREA-827	AREA-828	AREA-829	AREA-830	AREA-831	AREA-832	AREA-833	AREA-834	AREA-835	AREA-836	AREA-837	AREA-838	AREA-839	AREA-840	AREA-841	AREA-842	AREA-843	AREA-844	AREA-845	AREA-846	AREA-847	AREA-848	AREA-849	AREA-850	AREA-851	AREA-852	AREA-853	AREA-854	AREA-855	AREA-856	AREA-857	AREA-858	AREA-859	AREA-860	AREA-861	AREA-862	AREA-863	AREA-864	AREA-865	AREA-866	AREA-867	AREA-868	AREA-869	AREA-870	AREA-871	AREA-872	AREA-873	AREA-874	AREA-875	AREA-876	AREA-877	AREA-878	AREA-879	AREA-880	AREA-881	AREA-882	AREA-883	AREA-884	AREA-885	AREA-886	AREA-887	AREA-888	AREA-889	AREA-890	AREA-891	AREA-892	AREA-893	AREA-894	AREA-895	AREA-896	AREA-897	AREA-898	AREA-899	AREA-900	AREA-901	AREA-902	AREA-903	AREA-904	AREA-905	AREA-906	AREA-907	AREA-908	AREA-909	AREA-910	AREA-911	AREA-912	AREA-913	AREA-914	AREA-915	AREA-916	AREA-917	AREA-918	AREA-919	AREA-920	AREA-921	AREA-922	AREA-923	AREA-924	AREA-925	AREA-926	AREA-927	AREA-928	AREA-929	AREA-930	AREA-931	AREA-932	AREA-933	AREA-934	AREA-935	AREA-936	AREA-937	AREA-938	AREA-939	AREA-940	AREA-941	AREA-942	AREA-943	AREA-944	AREA-945	AREA-946	AREA-947	AREA-948	AREA-949	AREA-950	AREA-951	AREA-952	AREA-953	AREA-954	AREA-955	AREA-956	AREA-957	AREA-958	AREA-959	AREA-960	AREA-961	AREA-962	AREA-963	AREA-964	AREA-965	AREA-966	AREA-967	AREA-968	AREA-969	AREA-970	AREA-971	AREA-972	AREA-973	AREA-974	AREA-975	AREA-976	AREA-977	AREA-978	AREA-979	AREA-980	AREA-981	AREA-982	AREA-983	AREA-984	AREA-985	AREA-986	AREA-987	AREA-988	AREA-989	AREA-990	AREA-991	AREA-992	AREA-993	AREA-994	AREA-995	AREA-996	AREA-997	AREA-998	AREA-999	AREA-1000
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TABLE XV
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG
CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSV-Z
5	X-YTSVI-Z
	X-YTSVIT-Z
	X-YTSVITI-Z
	X-YTSVITIE-Z
	X-YTSVITIEL-Z
	X-YTSVITIELS-Z
	X-YTSVITIELSN-Z
10	X-YTSVITIELSNI-Z
	X-YTSVITIELSNIK-Z
	X-YTSVITIELSNIKE-Z
	X-YTSVITIELSNIKEN-Z
	X-YTSVITIELSNIKENK-Z
	X-YTSVITIELSNIKENKC-Z
	X-YTSVITIELSNIKENKCN-Z
	X-YTSVITIELSNIKENKCNG-Z
15	X-YTSVITIELSNIKENKCNGT-Z
	X-YTSVITIELSNIKENKCNGTD-Z
	X-YTSVITIELSNIKENKCNGTDA-Z
	X-YTSVITIELSNIKENKCNGTDAK-Z
	X-YTSVITIELSNIKENKCNGTDAKV-Z
	X-YTSVITIELSNIKENKCNGTDAKVK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKL-Z
20	X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z
25	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z
30	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butylloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates,
5 polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butylloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVI
RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG
AMINO TRUNCATIONS

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
10	X-AVTELQLLMQST-Z
	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
15	X-ELDKYKNAVTELQLLMQST-Z
	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDP-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
 "X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxyl, dansyl, or
 30 T-butyloxycarbonyl; an acetyl group; a 9-
 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a
 35 T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid
conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVIII
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
15	X-QVNEKINQSLAFIRKSDELL-Z
	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-DPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-YDPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG
CARBOXY TRUNCATIONS

X-ITL-Z
 X-ITLN-Z
 X-ITLNN-Z
 5 X-ITLNNS-Z
 X-ITLNNSV-Z
 X-ITLNNSVA-Z
 X-ITLNNSVAL-Z
 X-ITLNNSVALD-Z
 X-ITLNNSVALDP-Z
 X-ITLNNSVALDPI-Z
 10 X-ITLNNSVALDPID-Z
 X-ITLNNSVALDPIDI-Z
 X-ITLNNSVALDPIDIS-Z
 X-ITLNNSVALDPIDISI-Z
 X-ITLNNSVALDPIDISIE-Z
 X-ITLNNSVALDPIDISIEL-Z
 X-ITLNNSVALDPIDISIELN-Z
 X-ITLNNSVALDPIDISIELNK-Z
 15 X-ITLNNSVALDPIDISIELNKA-Z
 X-ITLNNSVALDPIDISIELNKAK-Z
 X-ITLNNSVALDPIDISIELNKAKS-Z
 X-ITLNNSVALDPIDISIELNKAKSD-Z
 X-ITLNNSVALDPIDISIELNKAKSDL-Z
 X-ITLNNSVALDPIDISIELNKAKSDLE-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEE-Z
 20 X-ITLNNSVALDPIDISIELNKAKSDLEES-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z
 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z
 25 X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxy, dansyl, or
 T-butyloxycarbonyl; an acetyl group; a 9-
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a
 T-butyloxycarbonyl group; a macromolecular carrier
 group including but not limited to lipid-fatty acid
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XX
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-TLNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XXI
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG
CARBOXY TRUNCATIONS

- X-ALG-Z
 X-ALGV-Z
 X-ALGVA-Z
 5 X-ALGVAT-Z
 X-ALGVATS-Z
 X-ALGVATSA-Z
 X-ALGVATSAQ-Z
 X-ALGVATSAQI-Z
 X-ALGVATSAQIT-Z
 X-ALGVATSAQITA-Z
 10 X-ALGVATSAQITAA-Z
 X-ALGVATSAQITAAV-Z
 X-ALGVATSAQITAAVA-Z
 X-ALGVATSAQITAVAL-Z
 X-ALGVATSAQITAVALV-Z
 X-ALGVATSAQITAVALVE-Z
 X-ALGVATSAQITAVALVEA-Z
 X-ALGVATSAQITAVALVEAK-Z
 15 X-ALGVATSAQITAVALVEAKQ-Z
 X-ALGVATSAQITAVALVEAKQA-Z
 X-ALGVATSAQITAVALVEAKQAR-Z
 X-ALGVATSAQITAVALVEAKQARS-Z
 X-ALGVATSAQITAVALVEAKQARSD-Z
 X-ALGVATSAQITAVALVEAKQARSDI-Z
 X-ALGVATSAQITAVALVEAKQARSDIE-Z
 20 X-ALGVATSAQITAVALVEAKQARSDIEK-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKL-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKLK-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKLKE-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKLKEA-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKLKEAI-Z
 X-ALGVATSAQITAVALVEAKQARSDIEKLKEAIR-Z
- 25 The one letter amino acid code is used.

Additionally,
 "X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxyl, dansyl, or
 T-butyloxycarbonyl; an acetyl group; a 9-
 fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a
 T-butyloxycarbonyl group; a macromolecular carrier
 group including but not limited to lipid-fatty acid
 conjugates, polyethylene glycol, or carbohydrates.
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TABLE XXII
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNCGTDAKVKLIKQELDKYKN-Z
 X-SVITIELSNIKENKCNCGTDAKVKLIKQELDKYKNA-Z
 5 X-VITIELSNIKENKCNCGTDAKVKLIKQELDKYKNAV-Z
 X-VAVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVS-Z
 X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSV-Z
 X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVL-Z
 X-SKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLT-Z
 X-KVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLTS-Z
 X-LEGEVNKIALLLSTNKAVVSLSNGVSVLTISKVLD-Z
 10 X-GEVNKIALLLSTNKAVVSLSNGVSVLTISKVLDLK-Z
 X-EVNKIALLLSTNKAVVSLSNGVSVLTISKVLDLKN-Z
 X-VNKIALLLSTNKAVVSLSNGVSVLTISKVLDLKNY-Z
 X-NKIALLLSTNKAVVSLSNGVSVLTISKVLDLKNYI-Z
 X-KIALLLSTNKAVVSLSNGVSVLTISKVLDLKNYID-Z
 X-IALLSTNKAVVSLSNGVSVLTISKVLDLKNYIDK-Z
 X-ALLSTNKAVVSLSNGVSVLTISKVLDLKNYIDKQ-Z
 X-VAVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVS-Z
 15 X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSV-Z
 X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVL-Z
 X-SKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLT-Z
 X-KVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLTS-Z
 X-LEGEVNKIALLLSTNKAVVSLSNGVSVLTISKVLD-Z
 X-GEVNKIALLLSTNKAVVSLSNGVSVLTISKVLDLK-Z
 X-EVNKIALLLSTNKAVVSLSNGVSVLTISKVLDLKN-Z
 20 X-VNKIALLLSTNKAVVSLSNGVSVLTISKVLDLKNY-Z
 X-NKIALLLSTNKAVVSLSNGVSVLTISKVLDLKNYI-Z
 X-KIALLLSTNKAVVSLSNGVSVLTISKVLDLKNYID-Z
 X-IALLSTNKAVVSLSNGVSVLTISKVLDLKNYIDK-Z
 X-ALLSTNKAVVSLSNGVSVLTISKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAQSDLEESKEWIRRSN-Z
 X-LNNSVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z
 X-NNSVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z
 X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z
 X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z
 X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDZ-Z
 X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDZI-Z
 30 X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDZIG-Z
 X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDZIGN-Z
 X-PIDISIELNKAQSDLEESKEWIRRSNQKLDZIGNW-Z
 X-IDISIELNKAQSDLEESKEWIRRSNQKLDZIGNWH-Z
 X-DISIELNKAQSDLEESKEWIRRSNQKLDZIGNWHQ-Z
 X-ISIELNKAQSDLEESKEWIRRSNQKLDZIGNWHQS-Z
 X-SIELNKAQSDLEESKEWIRRSNQKLDZIGNWHQSS-Z
 X-IELNKAQSDLEESKEWIRRSNQKLDZIGNWHQSSST-Z
 35 X-ELNKAQSDLEESKEWIRRSNQKLDZIGNWHQSSSTT-Z
 X-TAAVALVEAKQARSIDIEKLKEAIRDITNKAVQSVQS-Z

X-AVALVEAKQARSDIEKLKEAIRD TNKAVQSVQSSI-Z
 X-LVEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNL-Z
 X-VEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLI-Z
 X-EAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIV-Z
 X-AKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVA-Z
 X-KQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAI-Z
 X-QARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIK-Z
 5 X-ARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKS-Z
 X-RSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKSV-Z
 X-SDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIKSVQ-Z
 X-KLKEAIRD TNKAVQSVQSSIGNLIVAIKSVQDYVN-Z
 X-LKEAIRD TNKAVQSVQSSIGNLIVAIKSVQDYVNVK-Z
 X-AIRD TNKAVQSVQSSIGNLIVAIKSVQDYVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWERKVD FLEENITALL EEAQIQQ EKNMYELQK-Z
 X-QEWERKVD FLEENITALL EEAQIQQ EKNMYELQKL-Z
 X-EWERKVD FLEENITALL EEAQIQQ EKNMYELQKLN-Z
 X-WERKVD FLEENITALL EEAQIQQ EKNMYELQKLNS-Z
 X-ERKVD FLEENITALL EEAQIQQ EKNMYELQKLNSW-Z
 X-RKVD FLEENITALL EEAQIQQ EKNMYELQKLNSWD-Z
 15 X-KVD FLEENITALL EEAQIQQ EKNMYELQKLNSWDV-Z
 X-VDFLEENITALL EEAQIQQ EKNMYELQKLNSWDVF-Z
 X-DFLEENITALL EEAQIQQ EKNMYELQKLNSWDVFG-Z
 X-FLEENITALL EEAQIQQ EKNMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDLGPPISLERLDVGTNLGNIAIAKLEAKELL-Z
 X-HRIDLGPPISLERLDVGTNLGNIAIAKLEAKELLE-Z
 X-RIDLGPPISLERLDVGTNLGNIAIAKLEAKELLES-Z
 X-IDLGPPISLERLDVGTNLGNIAIAKLEAKELLESS-Z
 X-DLGPPISLERLDVGTNLGNIAIAKLEAKELLESSD-Z
 X-LGPPISLERLDVGTNLGNIAIAKLEAKELLESSDQ-Z
 X-GPPISLERLDVGTNLGNIAIAKLEAKELLESSDQI-Z
 25 X-PPISLERLDVGTNLGNIAIAKLEAKELLESSDQIL-Z
 X-PISLERLDVGTNLGNIAIAKLEAKELLESSDQILR-Z
 X-SLERLDVGTNLGNIAIAKLEAKELLESSDQILRSM-Z
 X-LERLDVGTNLGNIAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,
 "X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxy, dansyl, or
 T-butyloxycarbonyl; an acetyl group; a 9-
 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, et al., 1989, *Molecular Cloning*, A Laboratory Manual, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butyloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,
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below, and assays for antiviral activity are described in Section 5.5.2, below.

5.5.1 ASSAYS FOR CELL FUSION EVENTS

5 Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

10 Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus
15 that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each
20 peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used.
25 After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as
30 crystal violet stain, may be used to facilitate the visualization of syncytial formation.

5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

35 The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

easily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4⁺ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4⁺ cells by cell-free HIV. Such an assay may comprise culturing an appropriate

concentration (i.e., TCID₅₀) of virus and CD-4⁺ cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10^4 to 10^5 pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5 With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10 These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not
15 limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be
20 inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B
25 viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses
30 and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides
35 form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4⁺ cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and
35 small organic or inorganic molecules. Synthetic compounds, natural products, and other sources of

potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing,
5 for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178
10 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

15 In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time
20 sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide,
25 thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

30 (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and
35

(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches
5 that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate
10 wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled,
15 either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface
20 with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and
25 stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g.,
30 by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of
35 label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or
5 indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or
10 DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored
15 complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

20 Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107
25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

30 The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two
35 peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

been formed. The various formats are described briefly below.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding
5 partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent
10 attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

15 In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes
20 formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface
25 indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be
30 directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

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Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41A178 peptides and by assaying test

compounds for the disruption of the complexes formed by these two peptides by immunometrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test
15 compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be
20 conducted. Test compounds showing an ability to disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand or inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a
35 solid support such as a microtiter well. DP178

binding to M41A178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to
5 M41A178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178
10 (nonspecific).

5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct
intraventricular, intravenous, intraperitoneal,
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration
35 of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above.

5 Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external
10 microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

15 Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-
20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs
25 are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley
30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as
therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in
35 previously uninfected individuals after acute exposure

to an HIV virus. Examples of such prophylactic use of the peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents
5 in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the
10 invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may
15 prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in
20 amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀
25 (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds
30 which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of
35 circulating concentrations that include the ED₅₀ with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated
5 initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic
10 event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels
15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the
20 invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides
25 effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using
30 standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable
35 adjuvant in order to enhance the immunological

response. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydroxide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and *Corynebacterium parvum*. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated
35

for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

added, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be
5 used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or
10 dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a
15 plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In
20 soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

25 6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the
30 fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1)
35 shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

6.1. MATERIALS AND METHODS

6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H₂O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15 μ spherical) with a linear gradient; H₂O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35

6.1.2. VIRUS

The HIV-1_{LA1} virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640
5 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 μ m filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25 μ l of
10 serial diluted virus was added to 75 μ l AA5 cells at a concentration of 2×10^5 /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post
15 infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID₅₀ was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497).
20 The titer of the HIV-1_{LA1} and HIV-1_{MAN} stocks used for these studies, as measured on the AA5 cell line, was approximately 1.4×10^6 and 3.8×10^4 TCID₅₀/ml, respectively.

6.1.3. CELL FUSION ASSAY

25 Approximately 7×10^4 Molt cells were incubated with 1×10^4 CEM cells chronically infected with the HIV-1_{LA1} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100 μ l culture medium as previously described
30 (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10 μ l and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated
35 giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

6.1.4. CELL FREE VIRUS INFECTION ASSAY

5 Synthetic peptides were incubated at 37°C with
either 247 TCID₅₀ (for experiment depicted in FIG. 2),
or 62 TCID₅₀ (for experiment depicted in FIG.3) units
of HIV-1_{LA1} virus or 25 TCID₅₀ units of HIV-2_{NDH2} and CEM
CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4,
10 4.0, and 40µg/ml for 7 days. The resulting reverse
transcriptase (RT) activity in counts per minute was
determined using the assay described, below, in
Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J.
Hyg. 27: 493-497 for an explanation of TCID₅₀
calculations.

15

6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was
adapted from Goff et al. (Goff, S. et al., 1981, J.
Virol. 38:239-248) and Willey et al. (Willey, R. et
20 al., 1988, J. Virol. 62:139-147). Supernatants from
virus/cell cultures are adjusted to 1% Triton-X100. A
10µl sample of supernatant was added to 50µl of RT
cocktail in a 96-well U-bottom microtitre plate and
the samples incubated at 37°C for 90 min. The RT
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM
MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01),
0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-
01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-
radioactive dTTP, and 10µCi/ml ³²P-dTTP (Amersham, cat.
30 No. PB.10167).

After the incubation period, 40µl of reaction
mixture was applied to a Schleicher and Schuell (S+S)
NA45 membrane (or DE81 paper) saturated in 2 x SSC
buffer (0.3M NaCl and 0.003M sodium citrate) held in a
35 S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 μ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

6.2. RESULTS

10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 μ g/ml and 12.5ng/ml were tested for blockade of the
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1_{LAI}, HIV-1_{MN}, HIV-1_{RF}, or HIV-1_{SP2} virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV_{LAI} inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 μ g/ml (FIG. 4). These observations
35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptide/protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5 The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SP2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

10 The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

35

6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4⁺ CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1_{LAI} isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. *et al.*, 1992, Proc. Natl. Acad. Sci. USA **89**:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 µg/ml) of peptide was incubated with 247 TCID₅₀ units of HIV-1_{LAI} virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC₅₀=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC₅₀ concentrations of approximately 5 µg/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{LAI} or HIV-2_{NIH2}. 62 TCID₅₀ HIV-1_{LAI} or 25 GCID₅₀ HIV-2_{NIH2} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC₅₀ of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC₅₀ for HIV-2_{NIH2}, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

10

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

Approximately 3.8×10^5 CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

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7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

35

The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40 μ g/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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TABLE XXIV

5	Peptide	Peptide Concentration $\mu\text{g/ml}$	% Viability at time (hours)			
			0	24	48	72
10	DP178 (SEQ ID:1)	40	98	97	95	97
		10	98	97	98	98
		2.5	98	93	96	96
15	DP116 (SEQ ID:9)	40	98	95	98	97
		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107

Soluble recombinant forms of gp41 used in the
 example described below provide evidence that the
 DP178 peptide associates with a distal site on gp41
 whose interactive structure is influenced by the DP107
 leucine zipper motif. A single mutation disrupting
 the coiled-coil structure of the leucine zipper domain
 transformed the soluble recombinant gp41 protein from
 an inactive to an active inhibitor of HIV-1 fusion.
 This transformation may result from liberation of the
 potent DP178 domain from a molecular clasp with the
 leucine zipper, DP107, determinant. The results also
 indicate that the anti-HIV activity of various gp41
 derivatives (peptides and recombinant proteins) may be

due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

8.1. MATERIALS AND METHODS

5 8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of
10 gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer
15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's
20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41Δ107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'-
25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the
30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41-
35 PA178. All inserted sequences and mutated residues

were checked by restriction enzyme analysis and confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5 The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide
10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,
15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed
20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells (7×10^4) were incubated with HIV-1_{MB} chronically infected CEM cells
30 (10^4) in 96-well flat-bottomed half-area plates (Costar) in 100 μ l culture medium. Peptide and fusion proteins at various concentrations in 10 μ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated
35 with microscopic examination. Both M41 and M41-P did

not show cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO₃, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H₂O₂ were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H₂SO₄ after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

5 As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because 10 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely 15 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind 20 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant 25 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix 30 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein 35

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic
10 peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as
15 high as 50 μ M (Table XXV, below).

TABLE XXV

**DISRUPTION OF THE LEUCINE ZIPPER OF
GP41 FREES THE ANTI-HIV MOTIF**

20		<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
	Cell fusion (IC ₅₀)	1 μ M	1 nM	> 50 μ M	83 nM	> 50 μ M
25	Fab-D binding (K _D)	-	-	3.5x10 ⁻⁹	2.5x10 ⁻⁸	-
	HIV infectiv- ity (IC ₅₀)	1 μ M	80 nM	> 16 μ M	66 nM	> 8 μ M

30 1 The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

35

Antiviral Infectivity Assays. 20 μ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20 μ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 μ l of CEM4 cells at 6×10^5 cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₅₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

10

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1_{MB} infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 Δ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

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the DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED
IDENTIFICATION OF DP107-LIKE
AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs were tailored to the DP107 and DP178 sequences by

deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in
 5 FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 10 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A
 20 position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except
 25 C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in
 30 FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28
 35 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

35

Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped or glycoprotein sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein sequence names and motif hit locations for all the motifs searched.

5

10. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107 AND DP178-LIKE SEQUENCES
IN HUMAN IMMUNODEFICIENCY VIRUS**

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is

at the very C-terminus of gp120, just upstream of the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that
 5 the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite
 10 the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
 15 OF DP107-LIKE AND DP178-LIKE
SEQUENCES IN HUMAN RESPIRATORY
SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF_
 20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with
 25 similarities to DP-178, one just downstream of what would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTI5 also finds three areas including amino acids
 30 116-202, 267-302, and 506-549. The proline-leucine zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions
 35 which share location similarities with DP-178 of HIV-1.

12. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP107-LIKE AND DP178-LIKE SEQUENCES
IN SIMIAN IMMUNODEFICIENCY VIRUS**

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107-like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP107-LIKE AND DP178 LIKE SEQUENCES
IN CANINE DISTEMPER VIRUS**

Canine Distemper Virus (strain Onderstepoort) fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23). Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residues 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP107-LIKE AND DP178-LIKE SEQUENCES
IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107-LIKE AND DP178-LIKE
SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTI5 exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits nearer the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are
5 also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68)
15 at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell
20 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue
25 stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

In the Example presented herein, respiratory
30 syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on
35 the peptides, as discussed below. It is demonstrated

that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a
10 Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from A_{220} using Edlehoch's method (1967, Biochemistry 6:1948).

15

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse
20 and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

25

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes
30 at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

35

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD_{430/690} was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

5 3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC₅₀ data for each peptide represents the average of several experiments conducted utilizing that peptide.

17.2 RESULTS

20 The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC₅₀ values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their low IC_{50} values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS
TYPE 3 DP178/DP107 ANALOGS: CD AND
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses
35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were
5 determined from A_{210} using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of Hep2 cells chronically infected
10 with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing
35 uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500µg/ml to approximately

500ng/ml. For each of the assays, a well containing no peptide was also used.

18.2 RESULTS

5 The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC_{50} values. In fact, peptides 201 to 205 exhibit IC_{50} values in the nanogram/ml
20 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

25 Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

30 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289.
35 The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN EPSTEIN-BARR
VIRUS**

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr
5 is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus
10 predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor
15 (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas
20 algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is
25 a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a
30 homodimer.

Search results demonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found
35 between the known DNA binding and dimerization regions of the protein. Specifically, this region is located.

at amino acid residues 193-220, as shown in FIG. 33.
The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for
the fusion protein F1 of measles virus, strain
Edmonston (PC Gene® protein sequence PVGLF_MEASE),
successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at
10 amino acid residues 228-262. The ALLMOTI5 search
motif identifies three regions, including amino acid
residues 116-184, 228-269 and 452-500. Three regions
containing proline residues followed by a leucine
zipper-like sequence were found beginning at proline
15 residues 214, 286 and 451.

The Lupas program identified two regions it
predicted had potential for coiled-coil structure,
which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN HEPATITIS B
VIRUS

FIG. 35 depicts the results of a PZIP motif
search conducted on the Hepatitis B virus subtype AYW.
Two regions of interest within the major surface
25 antigen precursor S protein were identified. The
first lies just C-terminal to the proposed fusion
peptide of the major surface antigen (Hbs) which is
found at amino acid residues 174-191. The second
region is located at amino acid residues 233-267. The
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral
activity of these D178/DP107 analog regions, peptides
derived from area around the analog regions are
synthesized, as shown in FIG. 52A-B. These peptides
35 represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214).
Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

24. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN BACTERIAL
PROTEINS**

5 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

10 FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

15 FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

20 FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

25 FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS WITHIN VARIOUS
HUMAN PROTEINS**

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23L2IPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A_{280} using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (*i.e.*, cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for
5 addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E).
10 Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the
15 dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the
20 wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were
25 then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to
30 the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as
35 described above.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35µg/ml (T-257B1/C1) to 0.072µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

5 Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10

27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS:
 ANTIVIRAL CHARACTERIZATION

 In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides
15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral
20 capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis,
25 A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk
30 through the DP178-like region of the SIV TM protein.

 Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

35

27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified
10 viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP- 178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates.
25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 1) FIGS. 49A-C present peptides derived from
30 the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain
35 truncations of this region and/or mutations

which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5 2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated
10 in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

28.2 RESULTS

15 Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20 In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low IC_{50} values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50 represents a test peptide which contains a point
25 mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable antti-HIV-2 antiviral
30 activity.

 Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ($IC_{50} > 400 \mu g/ml$) whereas
35 the carboxy terminal peptide showed potent antiviral

activity (IC_{50} = 3 μ g/ml). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the
10 DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown
15 in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by
20 their low IC_{50} values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but
25 truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107
ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived
30 from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-
35 viral activity.

29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synthesized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a ³²P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

29.2 RESULTS

The EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

of the invention, and functionally equivalent methods and components are within the scope of the invention. Indeed, various modifications of the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the
5 foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

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WHAT IS CLAIMED IS:

1. An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.
5
2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
3. The peptide of Claim 2 in which the virus is
10 HIV-1 or HIV-2.
4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
5. The peptide of Claim 2 in which the virus is
15 a human parainfluenza virus.
6. The peptide of Claim 2 in which the virus is an influenza virus.
20
7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
8. The peptide of Claim 2 wherein the virus is
25 an Epstein-Barr virus.
9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide
30 recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
10. The method of Claim 9 wherein the virus is
35 HIV-1 or HIV-2.

11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

12. The method of Claim 9 wherein the virus is a human parainfluenza virus.

5

13. The method of Claim 9 wherein the virus is an influenza virus.

14. The method of Claim 9 in which the virus is a hepatitis B virus.

10

15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

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HIV1LA1 (DP-178; SEQ ID:1)	YTSLIHSLIEESNQQEKNEQELLELDKWASLWNWF
HIV1SF2 (DP-185; SEQ ID:3)	YTNTIYNLLEESNQQEKNEQELLELDKWASLWNWF
HIV1RF (SEQ ID:4)	YTGIIYNLLEESNQQEKNEQELLELDKWANLWNWF
HIV1MN (SEQ ID:5)	YTSIIYSLLEKSTQQEKNEQELLELDKWASLWNWF
HIV2ROD (SEQ ID:6)	LEANISKSLEQAQIQQEKNNYELQKLNWDIFGNWF
HIV2NIHZ (SEQ ID:7)	LEANISQSLEQAQIQQEKNNYELQKLNWDVFTNWL
DP180 (SEQ ID:2)	SSSFSTLLEQNNMKLQLAEQWLEQINEKHYLEDIS
DP118 (SEQ ID:10)	QQLLDVVKRQCEMLRLTVHGTKNLQARVTAIEKYLKDQ
DP125 (SEQ ID:8)	CCGNILLRAIEAQQHLLQLTVHGKQLQARILAVERYLKDQ
DP116 (SEQ ID:9)	LOARILAVERYLKDQQQ

FIG.1

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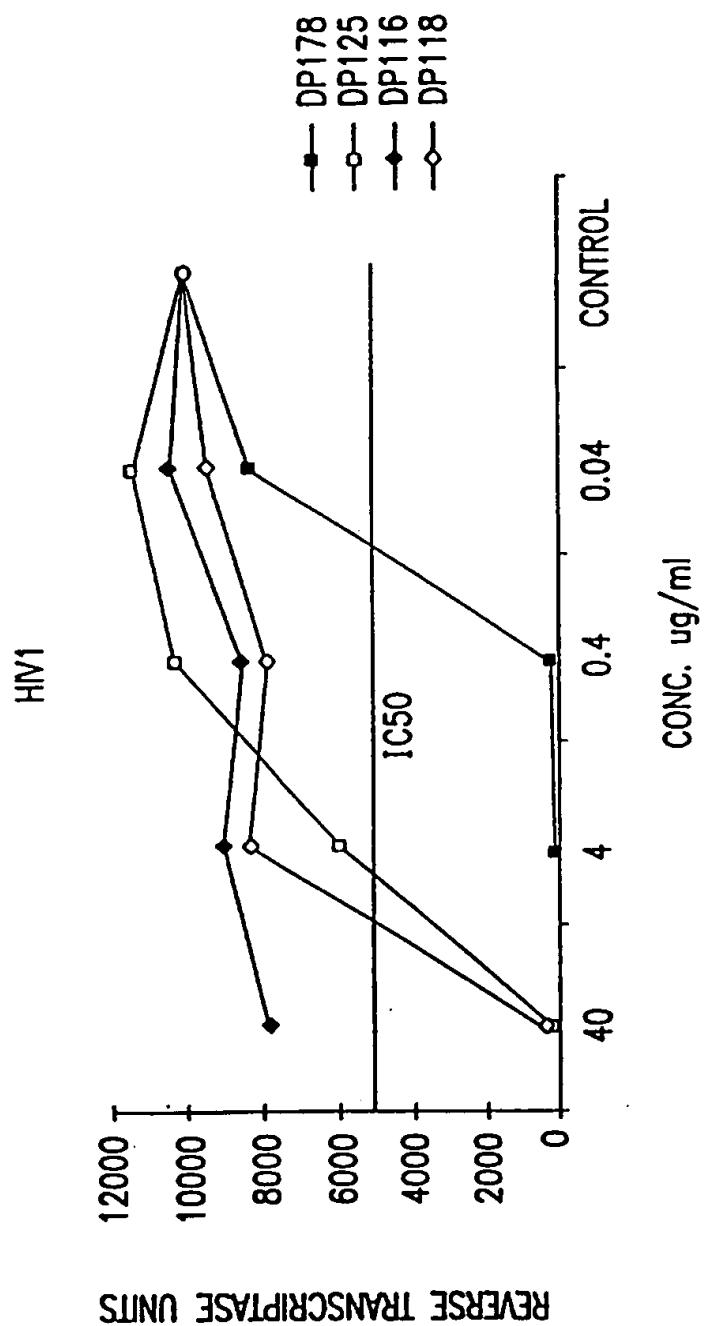


FIG.2

7872-020 (SHEET 3 OF 63)

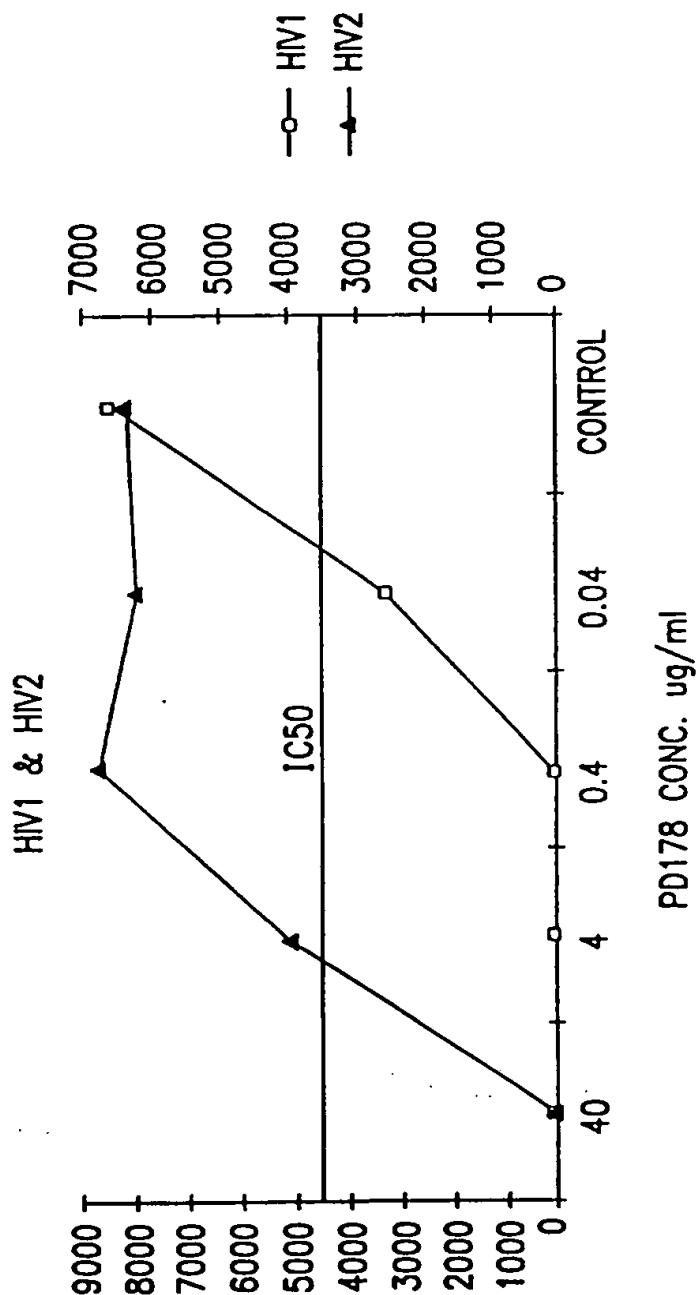


FIG.3

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Number of Syncytia/well: concentration in $\mu\text{g/ml}$ (micrograms/ml)									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAT	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAT	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LAT	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAT	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LAT	0	0	0	0	0	0	0	ND	60

FIG.4B

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<u>HIV1</u>								
Number of Syncytio/well: concentration in ng/ml (nanograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV1</u>	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV1</u>	ND	48	ND	ND	ND	ND	ND	ND
<u>HIV2</u>								
Number of Syncytio/well: concentration in μ g/ml (micrograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV2</u>	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV2</u>	ND	58	ND	ND	ND	ND	ND	ND

FIG.5

7872-020 (SHEET 6 OF 63)

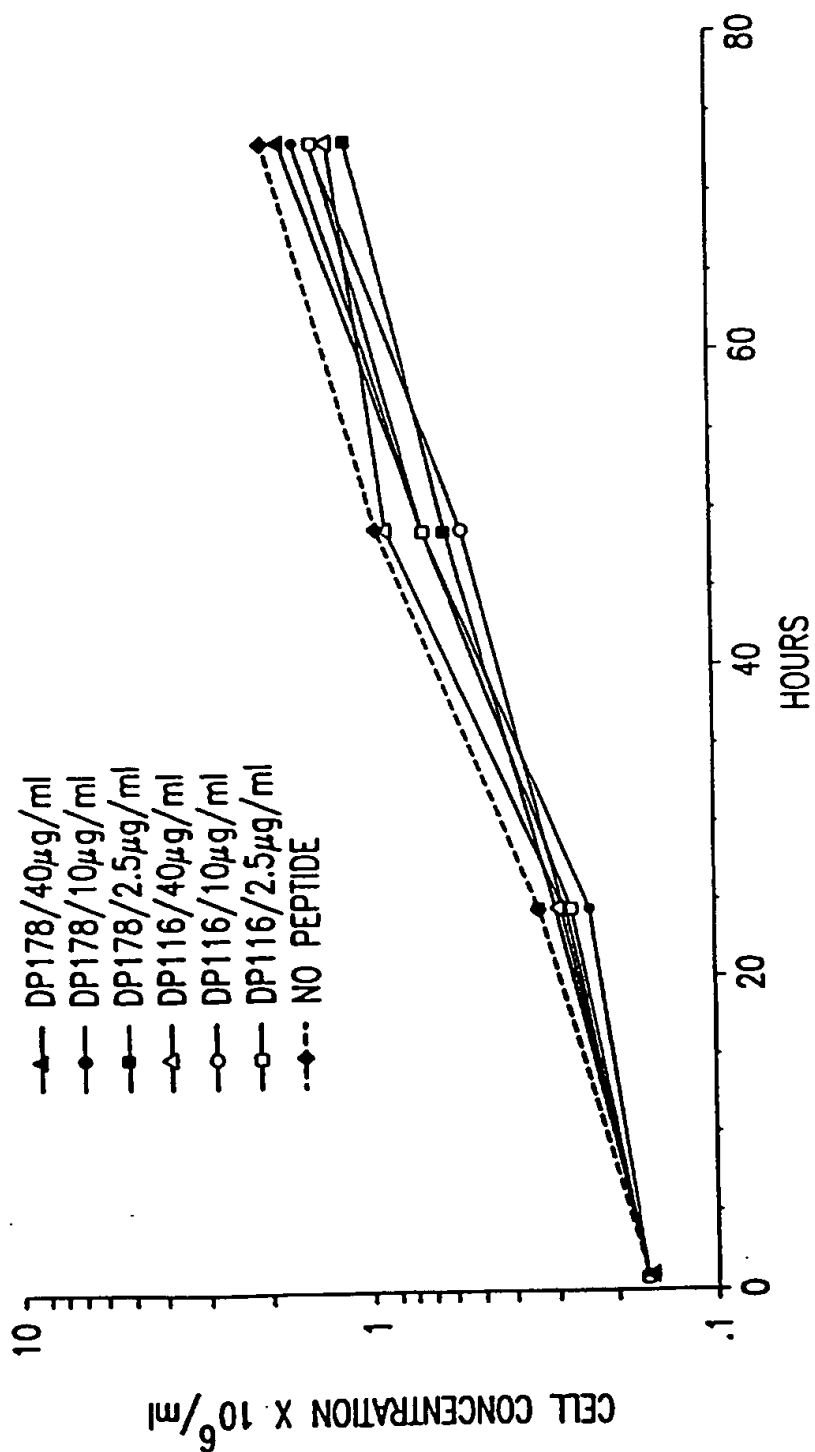


FIG.6

7872-020 (SHEET 7 OF 63)

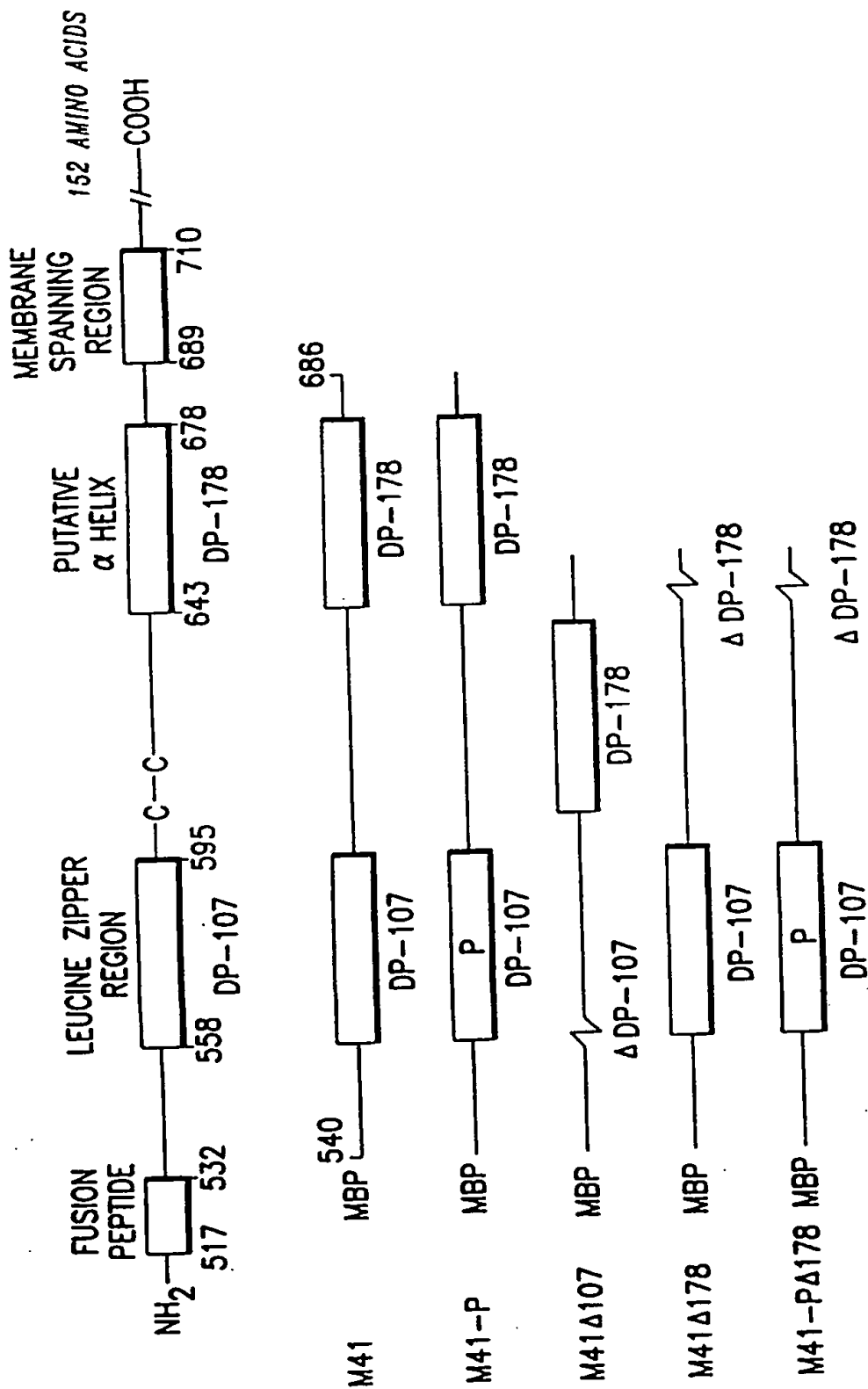


FIG.7

7872-020 (SHEET 8 OF 63)

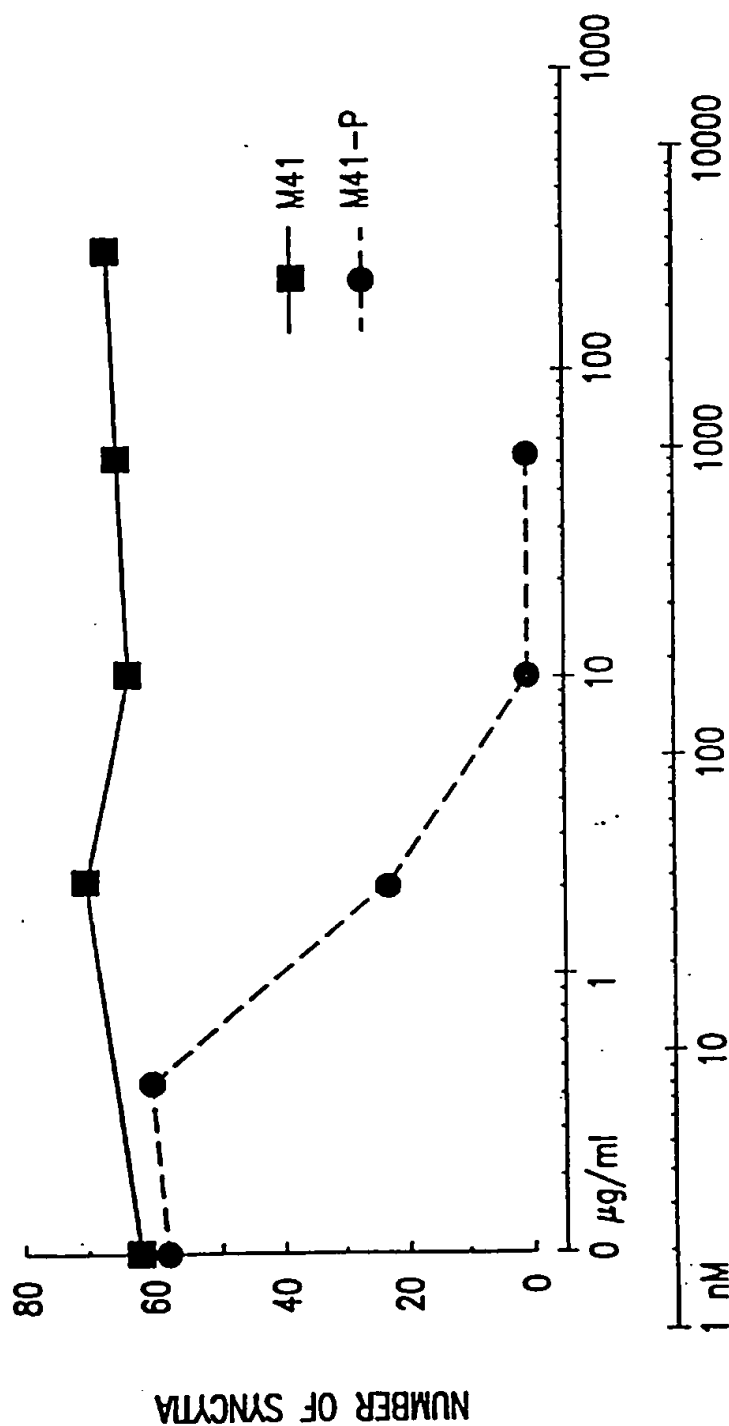


FIG.8

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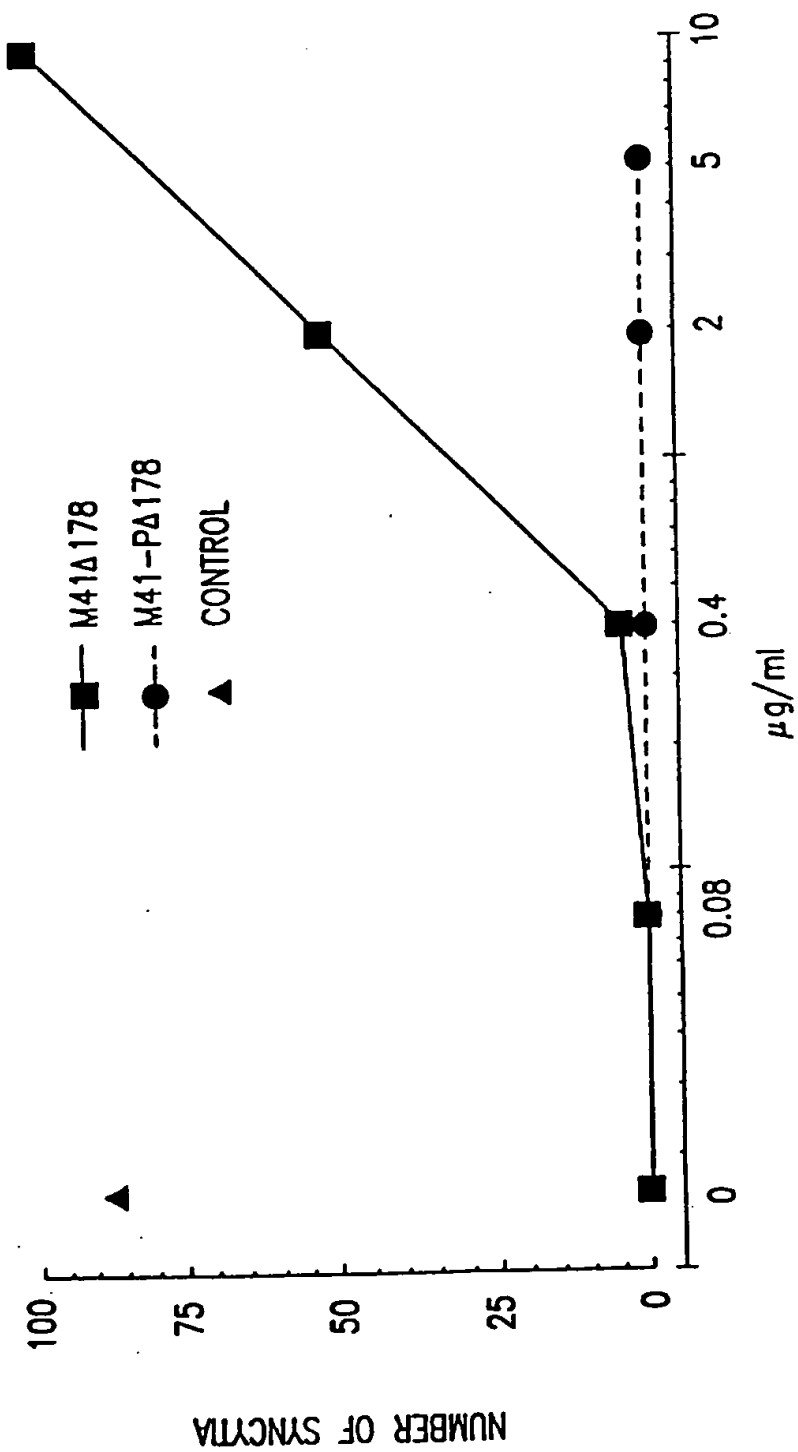


FIG.9

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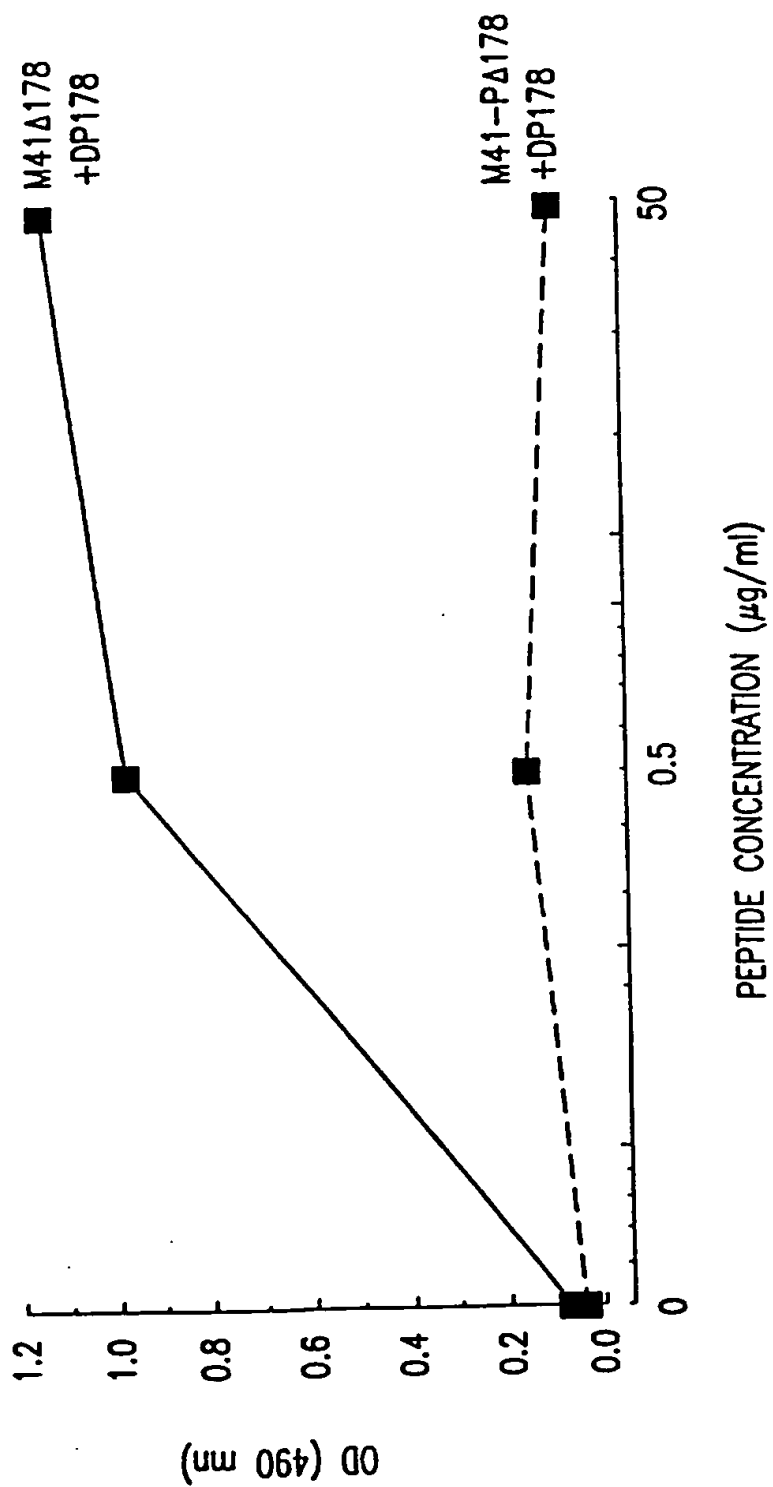
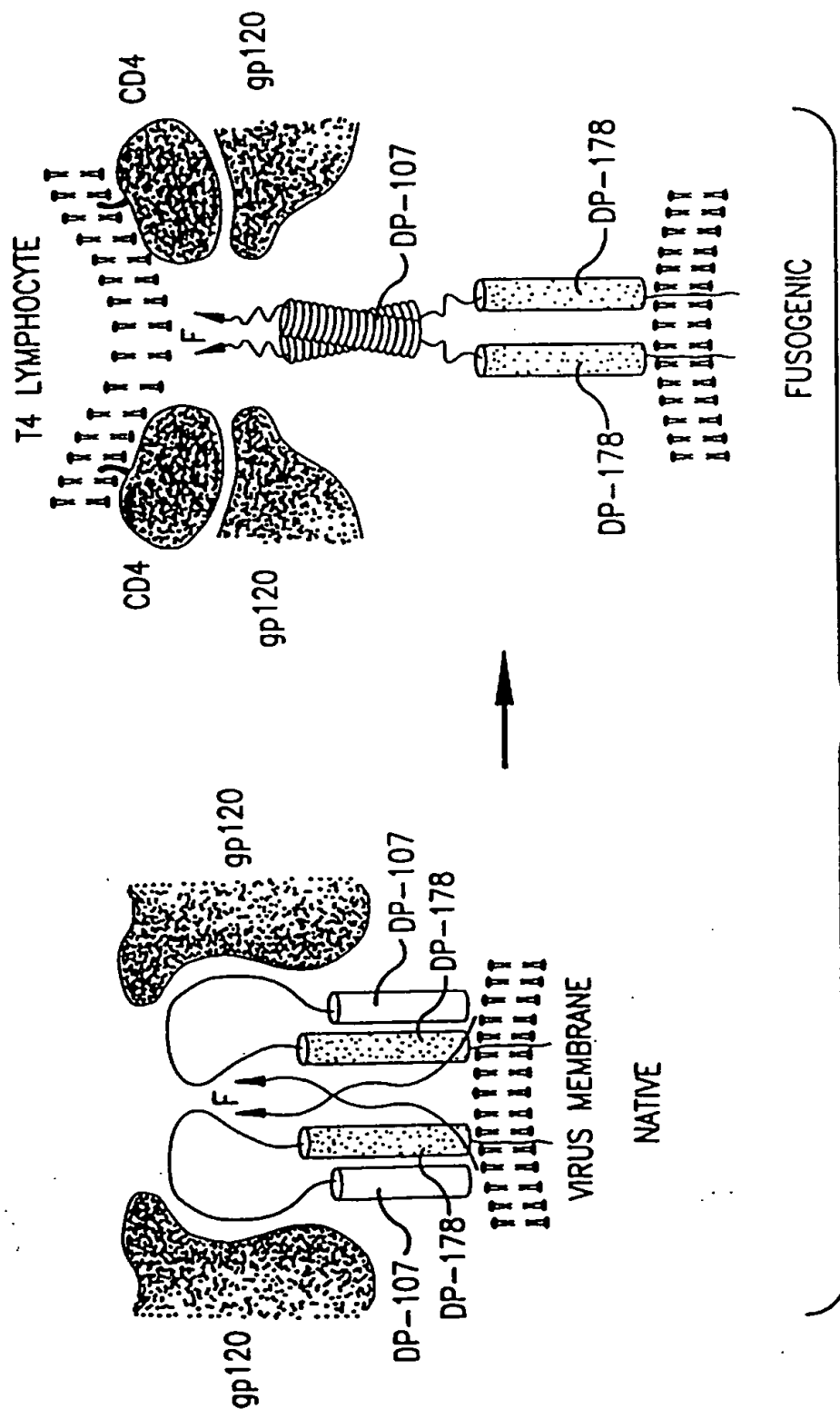
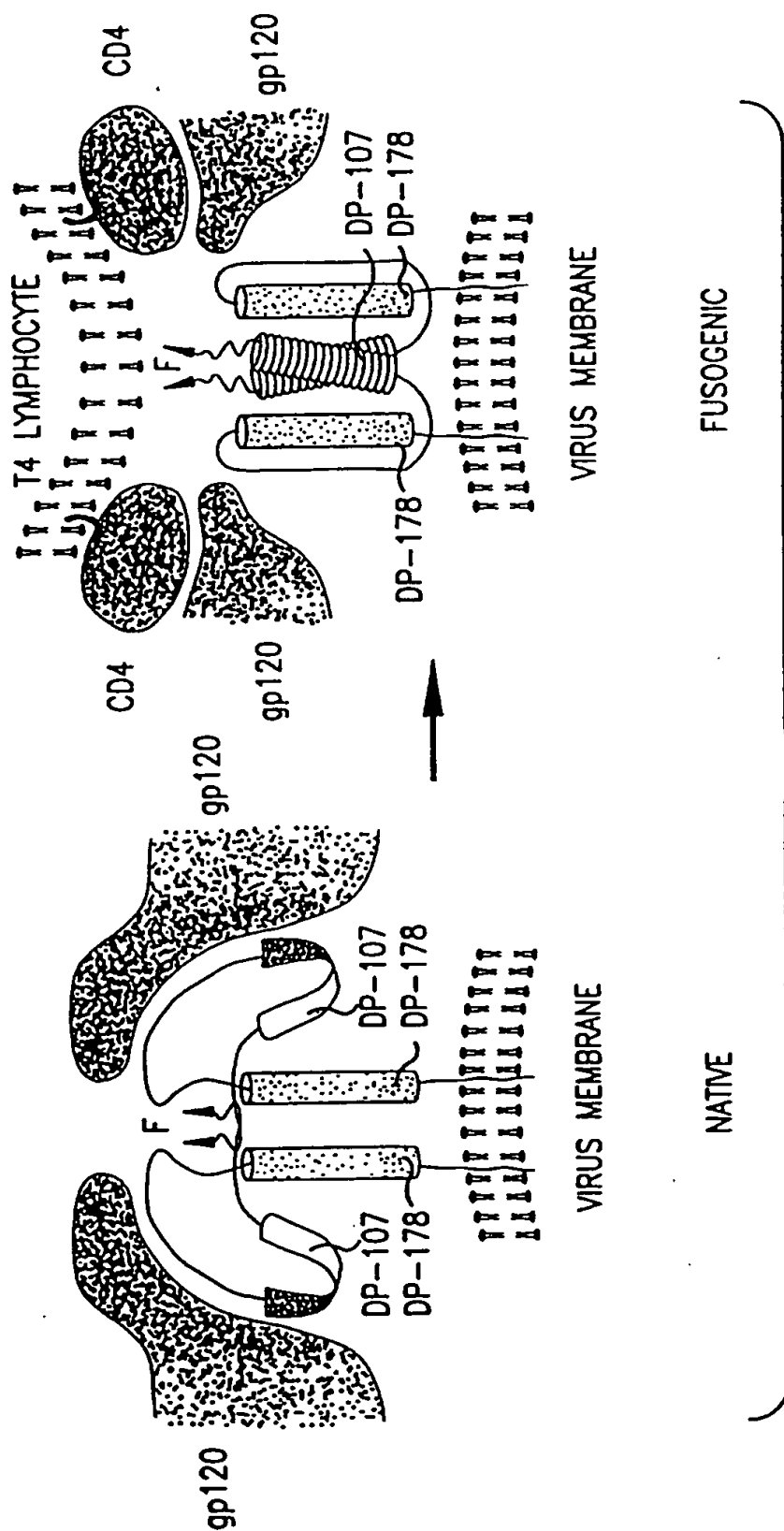


FIG.10

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Sequence	A	D	A	D	A	D	A	D	A	D	A	D	A	D	Motifs
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{ILOT} {CFIMPSTY}
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{ILOTV} {CDFIMPST}
DP-107 (env_hv1bru) L1=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{ILOTV} {CDFIMPST}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{EKLNOV} {CDFKMPSTY}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{EKLNOV} {CFKMPST}
DP-107 (env_hv1bru) L2=D	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	{EKLNOV} {CFKMPST}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EKLQY} {ACFGMPRWY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EKLQY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EFKLQWY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EILNQSY} {ACFGMPRWY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EILNQSWY} {CFGMPRVY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	{EFILNQSWY} {CFGMPRVY}

FIG.13

7872-020 (SHEET 16 OF 63)

Sequence	Positions												Parent Motif	Hybrid Motif			
	A	D	A	D	A	D	A	D	A	D	A	D					
GCN4 (gcN4 yeast)	W	K	Q	L	E	D	K	V	E	L	L	S	K	N	I	[L]A[V] [CFG]I[M]P[T]W	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]K[L]A[N]Q[V]Y [CFG]A[P]H	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]K[L]A[N]Q[V]Y [CFG]A[P]H	
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]K[L]A[N]Q[V]Y [CFG]A[P]H	
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]L[L]A[N]Q[S]V[Y] [CFG]A[P]H	
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]L[L]A[N]Q[S]V[Y] [CFG]A[P]H	
DP-178 (env_hv1bru)Y1=D	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	[E]F[L]A[N]Q[S]V[Y] [CFG]A[P]H	

FIG.15

7872-020 (SHEET 17 OF 63)

Sequence	Positions																								Parent Motif	Hybrid Motif											
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D													
DP-107 (env_hv1bru)L1=D	N	N	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	Q						
DP-107 (env_hv1bru)L2=D	N	N	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	Q						
DP-178 (env_hv1bru)Y1=A	Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F		
DP-178 (env_hv1bru)Y1=D					Y	T	S	L	I	H	S	L	I	E	E	S	Q	N	Q	E	K	N	E	Q	E	L	L	D	K	W	A	S	L	W	N	W	F
FLU LOOP 36	I	E	K	T	N	E	K	F	H	I	E	K	E	F	S	E	V	E	G	R	I	Q	D	L	E	K	Y										

</

FIG.16

Parent Motif {ILQTV} {CDFIMPST}
 {EKLNV} {CFKAPS}
 {EFKLWY} {CFGPRVY}
 {EFILNOSHY} {CFGLPRVY} {EFILNOSTWNY} {CFMP}
 {FILTV} {ACFLMPTVW}

7872-020 (SHEET 18 OF 63)

Sequence	Positions																Parent Motif	Hybrid Motif
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D		
GCN4 (gcN4 yeast)	MKQL	EDKV	EEL	LSKN	YHL	ENE	VAR	LKKL									{LMNV} {CFGIMP}TW	
DP-107 (env_hv1bru) L1=D	NNLL	RAIE	AQHL	LQLT	VWGI	IKQL	QAR	ILAV	EY	LKDQ							{ILOTV} {COFIMP}ST	
DP-178 (env_hv1bru) Y1=A	YTSL	IMSL	IEES	SNQD	QEKNE	QEL	LELD	OKWA	SLWN	WFF							{EFKLOWY} {CFGAPRVY}	{EFIKLNDQTVHY} {CFMP}
GCN4 (gcN4 yeast)	MKQL	EDKV	EEL	LSKN	YHL	ENE	VAR	LKKL									{LMNV} {CFGIMP}TW	
DP-107 (env_hv1bru) L1=D	NNLL	RAIE	AQHL	LQLT	VWGI	IKQL	QAR	ILAV	EY	LKDQ							{ILOTV} {COFIMP}ST	
DP-178 (env_hv1bru) Y1=A	YTSL	IMSL	IEES	SNQD	QEKNE	QEL	LELD	OKWA	SLWN	WFF							{EFILNDSHY} {CFGAPRVY}	{EFILNDQSTVHY} {CFMP}
GCN4 (gcN4 yeast)	MKQL	EDKV	EEL	LSKN	YHL	ENE	VAR	LKKL									{LMNV} {CFGIMP}TW	
DP-107 (env_hv1bru) L2=D	NNLL	RAIE	AQHL	LQLT	VWGI	IKQL	QAR	ILAV	EY	LKDQ							{EKLNDV} {CFKAPS}	
DP-178 (env_hv1bru) Y1=A	YTSL	IMSL	IEES	SNQD	QEKNE	QEL	LELD	OKWA	SLWN	WFF							{EFKLOWY} {CFGAPRVY}	{EFKLNQVHY} {CFMP}
GCN4 (gcN4 yeast)	MKQL	EDKV	EEL	LSKN	YHL	ENE	VAR	LKKL									{LMNV} {CFGIMP}TW	
DP-107 (env_hv1bru) L2=D	NNLL	RAIE	AQHL	LQLT	VWGI	IKQL	QAR	ILAV	EY	LKDQ							{EKLNDV} {CFKAPS}	
DP-178 (env_hv1bru) Y1=D	YTSL	IMSL	IEES	SNQD	QEKNE	QEL	LELD	OKWA	SLWN	WFF							{EFILNDSHY} {CFGAPRVY}	{EFIKLNDQSVHY} {CFMP}

FIG.17

7872-020 (SHEET 20 OF 63)

P-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{1}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{2}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{3}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{4}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{5}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{6}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{7}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{8}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{9}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-P{10}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-X{1,12}-[LIV]-P{6}-[LIV]-P{6}-[LIV]
P-X{13,23}-[LIV]-P{6}-[LIV]-P{6}-[LIV]

FIG.19

7872-020 (SHEET 21 OF 63)

Fusion Peptide \heartsuit ALLMOTIS \heartsuit
 \heartsuitELGELG A AGSTMGARSM TLTVQARQ \spadesuit 107x178x4 \spadesuit
 \spadesuit LLSGIVQQQ DP107-NNL

LRAIEAOOHL LOLT VWGIKO LOARILAYER YLKDO-DPI07 QLLG+V I WGC

SGKLICT TAVP ♡WNASWS NKSLEQIWNN MTWM ♡E ♡WDRELN DPI78-

YTSLHSL IEESONOOEK NEQELLELDK* WASLWNWE-DPI78 NI

◆ Transmembrane Region ◆
TNWLWYIK◆ ◆ IFIMIVGGLVGLRIVEAVLSIV NRVRQGYS♥ PL

†P23LZIPC†
SFQTHLPTPR GPDR †PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRLSL† CL

♥ALLMOTIS♥ ♠107x178x4♠
F ♥SYHRLRDLL LIVTRIVELL GRGW ♠EALKY WWNLOYWSQ

ELKNSAVSLLNAT⁺ ALAVAEG TDRVIEVVQG A⁺ CRAIRHPR

RIRQGLERIL L

FIG. 20

7872-020 (SHEET 22 OF 63)

Fusion Peptide
 ♡.....FLGFL ♡ALLMOTI5 ♡107x178x4
 ♡.....FLGFL LGVGSALAS GVA ♡YSKVLHL EGEVNIKIKSA

♡P1&12LZIPC ♡
LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ ♡ ♡ LL ♡PIVNKQ

♡107x178x4
 SC ♡SISNIETV I ♡ EEOQIKNNRLLETTREESYNAG ♡ VITPVSTMLTNSSELLSL

♡P1&12LZIPC ♡
 ♡ALLMOTI5 ♡
 INDM ♡PI ♡TNDQ KKLSMNNVQI V ♡ RQSYSI ♡ MS IIKEEVLAYV

VQ ♡ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

♡P7, 12, & 23LZIPC ♡
 ♡107x178x4 ♡ALLMOTI5 ♡
 EPIINFYDPLVF ♡PSDE ♡EDASISQVNEKINOSLAE ♡I ♡ RKSEDELL ♡

♡Transmembrane Region ♡
 HNVNA ♡ GK STTN ♡IMITLUVIVILLS LIAVGLLLY ♡ C ♡

KARSTPVTLS KDQLSGINNI AFSN

FIG. 21

7872-020 (SHEET 23 OF 63)

Fusion
Peptide ♡ALLMOTIS♡ ♡107x178x4♡
.....ELGELG ♡AAGTA MGAAA ♡TALTVQSOHLLAGILOQOKNLLAAY

 ♡107x178x4♡
EAQ ♡ QQM ♡ LKLTIWGYKNLNARVTALEKYLEDOARLN ♡ AWG ♡ CA

 ♡LYS Coiled-Coil♡
 ♡ALLMOTIS♡ ♡107x178x4♡
WKQVCHTTVP WQWNNRTPDW ♡NNMT ♡WLE ♡WEROISYLEGNTT

 ♡107x178x4♡
TOLEEARAQEEKNLD ♡ AYOKLSS ♡ WSDFWSW ♡ FDF ♡ SKWLN ♡ ILK

♡Transmembrane Region♡
IGELDYLGIGLRLLLYTV ♡ YS ♡ CIARVRQGYS PLSPQIHHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKS NWCK RL TNWCSISS IWL YNS

♡ALLMOTIS♡
♡CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♡

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22

7872-020 (SHEET 24 OF 63)

Fusion ♣ 107x178x4 ♣
 Peptide ♣ ALLMOTIS ♣ *LVS Coiled-Coil*
EAG ♣ VYL AGVALGVATA AQITAGIALHQ ♣ *SNLNAAQAIQ

SLRTSLEQSNKAIEEIREATOETVIA * VOGVQDY ♣ VNNEL ♣ VP

♣ ALLMOTIS ♣
 ♣ 107x178x4 ♣
 ♣ P6 & 12LZIPC ♣

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD ♣ PISA ♣ ♣ EISIQALIXAL

GGEIHKILEKLGYSGSD ♣ MIALESRGIKTKI ♣ THVDLPGKF ILSISY

♣ P1 & 12LZIPC ♣
 ♣ PTLSEVKGVIVHRLEAV ♣ SYNIGSQEWYTTVPRYIATNGYLISNFDDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil
 ♣ ALLMOTIS ♣
 ♣ P12 & 23LZIPC ♣

DMVYEGKVAL G ♣ PAISLD ♣ RL * DVGTNLGNALKKLDDAKVLI ♣

♣ Transmembrane Region ♣

DSS ♣ NOILETVR RS ♣ SFN ♣ EGSLLSVPILSCTAL ALLLLIYCC ♣

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

FIG. 23

7872-020 (SHEET 25 OF 63)

Fusion ♥ALLMOTIS♥

Peptide

♦107x178x4♦

♥.....FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ♦ILRLKESITATIEAVHIEVTDGLSOLAYA♦ VG KM♥ QQFVNDQFNNTAQELDCIKITQQV

♥ALLMOTIS♥

GVELNLYLTELT TV FGPQITSPAL ♥TQLTIQALYNAGGNMDYLLTKLGVG

♦P1 & 12LZIPC♦

NNQLSSLIGSGLIT GN♥ ♦PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVVTQVGSVI EELDTSYCIE TDL DLYCTRI VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGISQ

♥ALLMOTIS♥

♦107x178x4♦

NYGEAVSLID RHSCN ♦♥VLSLD GITRLSGEF DATYQKNISI LDSQVIVTG

LVS Coiled-Coil

♦Trans-*NLDISTELGNY NNSISNALDK LEESNSKLDK VNVKLTSTSA ♦LIT* YIAmembrane Region♦LTASLVCGJLSLV♥♦ LACYLMY♦ KQKAQQKTLLWLGNNTLGQMRATTKM

FIG. 24

7872-020 (SHEET 26 OF 63)

Fusion ♡ALLMOTIS♡
 Peptide ♡107x178x4♡ *LVS Coiled-Coil*
EEGGV ♡IG ♡TIALG *VATSAQITAAYALVEAKOARSDIEKLKE

AIRDTNKAVQSVQSSIGNLIVAIKSVQ* DYVNKE♡ ♡ IVPSIARLGCEAAG

 ♡ALLMOTIS♡
 ♡107x178x4♡
 LQLGIALTQH ♡♡YSELTNIEGDNIGSLOEKGIKLOGIASLYRTNITE♡ ♡

 ♡P5 & 12LZIPC♡
 IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL ♡PLLTRLNLTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

 ♡ALLMOTIS♡
 ♡107x178x4♡
 ♡P6 & 23LZIPC+
 NDITLNNVALD +PIDI ♡SIELN ♡KAKSDLEESKEWI+ RRSNOKL÷

 ♡Transmembrane Region+
DSIGNWHOSSTT ♡IIIIV+ LIMHLEHNTII+ ILAVKYY♡ R

IQKRNKRVLDQN DKPYVLTK

FIG. 25

7872-020 (SHEET 27 OF 63)

Fusion

Peptide

.....GLEGAI AGFIENGWEGMIDGWYGFRIHQNSEGTG

♣107x178x4♣

▼ALLMOTI5▼

LVS Coiled-Coil

Q ▼AADLKST ♣QAAIDQINGKLNRYIEKTNEKEHQIEKEESEVEGRIQDLEKYVEDTKIDL WSYNAELLYALENQHTI♣ DLT▼ DSEMKNLFETR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRCNIRCNICI

FIG. 26

7872-020 (SHEET 28 OF 63)

RV F2	AV	Purified KC10 (x - y)																CO
		(ug/ml)																
T-142	++																	++
T-143	++																	++
T-144	+																	+
T-145	++																	++
T-146	+																	+
T-147	+																	+
T-148	+																	+
T-149	+																	+
T-150	+																	+
T-151	+/																	+/
T-152	+/																	+/
T-153	+																	+
T-154	+/																	+/
T-155	+																	+

FIG. 27A

7872-020 (SHEET 31 OF 63)

RSV	Peptide #	AVG. IC ₅₀ (XTT) µg/ml
T-12	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	>500
T-13	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y	>500
T-15	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y	>500
T-19	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K V L D L K N Y	>500
T-26	A S Q V A V S K V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K	>500
T-28	S Q V A V S K V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K	327
T-30	V L H L E Q E V N K I K S A L L S T N K A V V S L S N Q V S V L T S K	328
T-69	V V S L S N Q V S V L T S K V L D L K N Y I D K Q L L	292
T-70	V N K I K S A L L S T N K A V V S L S N Q V S V L T S K	349
T-66	N D Q K K L M S N N V Q I V R Q Q S Y S I M S I I K E E	>500
T-576	S I S N I E T V I E F Q G K N N R L L E I T R E F S V N A Q V T T P V S	>100

FIG. 27D

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[illegible]

F16.28A

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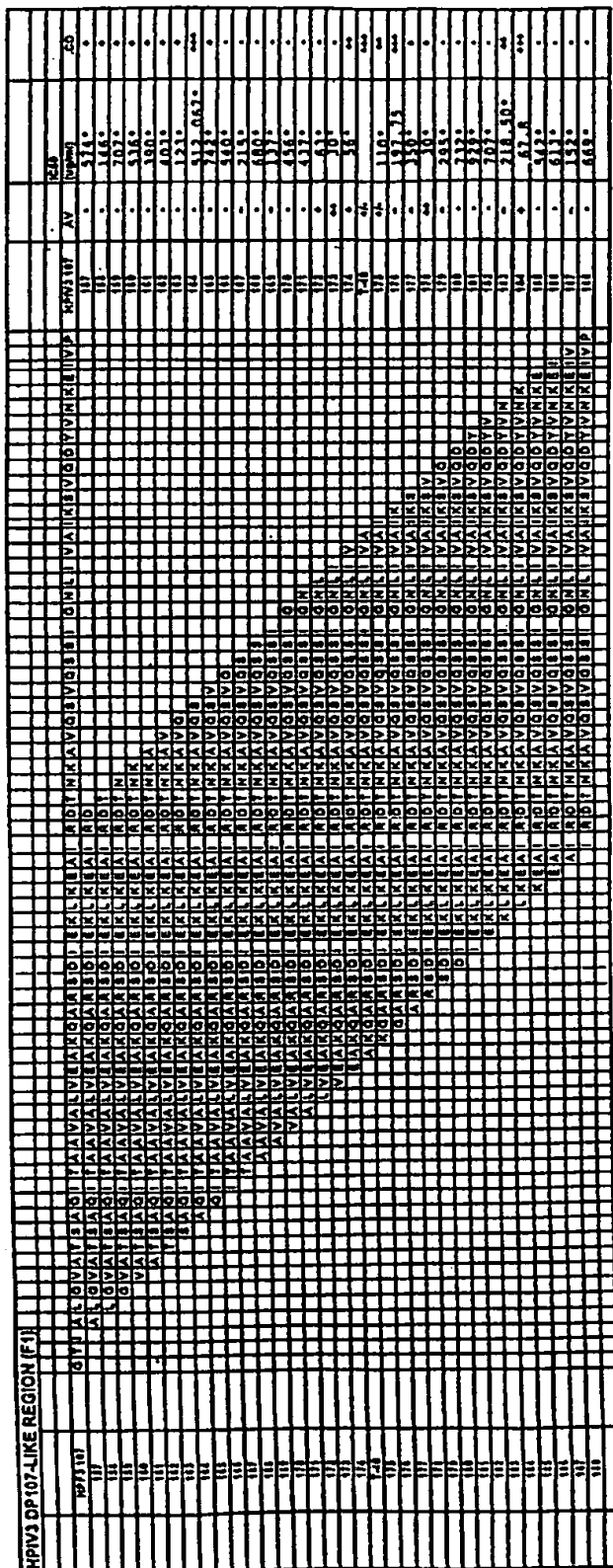


FIG. 29A

7872-020 (SHEET 35 OF 63)

HPV3 DP107 Line Walks		AVG. IC50	
T-42	A	T	843,000 ug/ml
T-43	A	T	853,000 ug/ml
T-39	A	T	720,000 ug/ml
T-38	A	T	702,000 ug/ml
T-40	A	T	54,793 ug/ml
T-44	A	T	228,140 ug/ml
T-45	A	T	488,000 ug/ml
T-46	A	T	648,000 ug/ml
T-502 Inactivated 184	L	K	137,554 ug/ml

29B

7872-020 (SHEET 36 OF 63)

PIV3 DP178-LIKE REGION (°F)																			
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220
221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260
261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320
321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380
381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420
421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440
441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460
461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480
481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500
501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520
521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540
541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560
561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580
581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600
601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620
621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640
641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660
661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680
681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700
701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720
721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740
741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760
761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780
781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800
801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820
821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840
841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860
861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880
881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900
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941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960
961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980
981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000

FIG. 30A

7872-020 (SHEET 38 OF 63)

Fusion

♥ALLMOTI5♥

Peptide

♠107x178x4♠

.....RNKRGVFLGLGFLATAGSAMGAAS ♠♥ XXXXAQSRTLLAGIVQQQQQLLDVVKROQELLRLTVWGTKNLOTRVTAIEKYLKDQAQL♠NAWG♥ CAF

♥ALLMOTI5♥

*LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND ♥TWQEWERKVD FLEENITALLEEAQIQQ

♠107x178x4♠

EKNMY ♠ELQKLNSWD* VF♥ GNXXXXXXXXXXXXXXXXXXXXXXXXXXXX♠

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP

WQIEYIHF

FIG. 31

7872-020 (SHEET 39 OF 63)

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSPFRVCELSSHGDLFRFSSD

♠107x178x4♠

IQCPSTGTRENTHEGLLMVFKDNIIPYSF ♠KVRSYTKIVTNILYNGWYADSVTNRHE♠

EKFSVDSY ETDQMDTIYQ CYNVVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTPNQ GERRAFLDKG TYTLWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPPTVMSSYI GKAVAAKRLG DVISVSQCVP VNQATVTLRK

SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TTKMTEVCQA TSQYYFQSGN

♠107x178x4♠

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ♠SLIENIDFASLELYSRDEQRASNVED ♠LE♠

LVS Predicted Coiled Coil

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

♠P12LZIPC♠

TM Potential

TM Potential

LVSTVGGLFSSLVSGFISF FK N ♠PFGGMLILVLVAGVVILVISL♠ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

FIG. 32

7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQQQ

LTAYHVSTAP TGSWFSAQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ ▲107x178x4▲ +Dimerization+
@KRY KNRVASRKCRAK ▲FK@ Q +LLOHYREVAAAKSSENDRLRLLLKQ▲

MCPSLDVD+ SI IPRTDVLHE DLLNF

FIG. 33

7872-020 (SHEET 41 OF 63)

Fusion

Peptide

FAG

♥ALLMOTIS♥

LVS Coiled-Coil

♥VVLAGAALGVATAAQITAGIALHQSMLENSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYNN♥ ELIPSMNQLSCDLIGQKLGLKLLRYYT

♣P23LZIPC♣

♣P6,12LZIPC♣

♣107x178x4♣

♥ALLMOTIS♥

EILSLFGPSLRD ♣PISA ♣♥EISIQALS~~Y~~ALGGDINKV♣ LEKLGYSGGDL♣

♣P1,12LZIPC♣

LGILES♣ RGIKARI♥ THVDTESYFIVLSIAY ♣PTLSEIKGVIVHRLEGV♣ SY

NIGSQEWYTTVPKYVATQGYLISNFEDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

♣P23LZIPC♣

♣P12LZIPC♣

♥ALLMOTIS♥

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS*LERLDVGTNLGN

♦Transmembrane Region♦

AIAKLEDAKELL♣ ESSDOI*L♣ RSMK ♦GLSSTSIVYILI♥ AVCLGGLIGIP

ALICCC♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

FIG. 34

7872-020 (SHEET 42 OF 63)

Pre S1 and Pre S2

MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

✦P12 & 23LZIPC✦

MENITSG FLG ✦PLL VLQAGFFLLTRILTI✦ PQSLDSWWTSLNFLGGTTVCLG

✦P12 & 23LZIPC✦

QNSQSPTSNHSPTSCPPTC ✦PGYRWMCLRRFIIFLFILLCLIFLLVLLDYQGML✦

PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPSSWAFGKF

♦Transmembrane Region♦LWEWASARFSWLS ♦LLVPEVQWFVGLSPTVWLSVI♦ WMMWYWGPSL♦Transmembrane Region♦♦YSILSPELPLLPFFCLWVYI♦

FIG. 35

7872-020 (SHEET 43 OF 63)

Fusion ♥ALLMOTI5♥ ♠107x178x4♠
Peptide *LVS Coiled Coil
AIQLIPLFVG LGI ♥TTAVSTGAAGLGVS ♠IT *QYTKLSHQLISDV

QAISSTIODLODQVDSLAEVVLO* NRRGLDLLTAE♠ QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....??.....

FIG 36

7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

♠107x178x4♠

♥ALLMOTI5♥

♠♥YODYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA♠ T♥

PK DTQYDIGFT

♠107x178x4♠

♥ALLMOTI5♥

♠♥ESTLLDGSQIQTVDNODGTVELVATLGKSSGS♠ AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

FIG. 37

7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

♠107x178x4♠

♥ALLMOTIS♥

♠♥KDNTSAGVASSSSIKGKYVKEVKVENGVTAT♠

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38

7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTTTLQN

CDPTTANGTA NKANKVGLYF Y

♠107x178x4♠

♥ALLMOTI5♥

♠♥SWKNVDKENNETLKNEQTTADYATNVNI♠

QLMESNGTKAISVVGKETE♥

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

FIG. 39

7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLLATT ATDFTPVP

♠107x178x4♠

♥ALLMOTI5♥

♠♥LSSNQIITAKASTNDNIKDLLDWYSSGSDTETNS♠♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSAPFTKGE KV

♠107x178x4♠

♠DLNTRTKKSOHTSEGTYIHFOISGVT♠

N TEKLPTPIEL PLKVKVHVKD SPLKYG

♣P12LZIPC♣

♣PKFDKKQLAISTLDFEIRHQLTQI♣

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40

7872-020 (SHEET 48 OF 63)

♥ALLMOTI5♥

MKKTAFILLL FIALTLTTSP L ♥VNG

♠107x178x4♠

LVS Predicted Coiled-Coil

S ♠EKSEEINEKDLRKKSELORNALSNLROIY YNEKAITENKESDD♠

QFLENTLL♥ FKG FFTGHPW

♠107x178x4♠

♠YNDLLVDLGSKDATNKYKGKKVDLYGAY♠

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEKKVP INLWIDGKQTTV

♣P12LZIPC♣

♣PIDKVKTSKKEVTVQELDL♣ QARHYLHGK FGLYNSDSFGGKVQ

♣P12LZIPC♣

RGLIVF HSSEGSTVSY DLFDAQGQY ♣P DTLRIYRDN KTINSENLHI♣

DLYLYTT

FIG. 41

7872-020 (SHEET 49 OF 63)

MKKTAFTLLL FIALTLTTSP L ♥ALLMOTIS♥
♥VNGS

♠107x178x4♠

♠EKSEEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHDA Q♥

FLQHTILFKG FFDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEKKVPINLWLDGKQNTV

♠107x178x4♠

♥ALLMOTIS♥

♣P12LZIPC♣

♣P ♥L ♠ETVKTNNKNVTVOELDLOARRYL♣ OEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

♣P23LZIPC♣

♣PSVNYDLFGAQQQYSNTLLRIYRDNKTINSENMI♣ DIYLYTS

FIG. 42

7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

♥ALLMOTIS♥

♥QMNINLYDHARGTQTGFVRYDDGYV

♠107x178x4♠

♠STSLSLRSAHLAQYILSGYSLTIYIVI♠ ANMFNVNDVISVY♥

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ALLMOTIS♥

♥ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL♥

FIG. 43

7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSTYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLQPA

LVSSVAPSQT RAPHFPGVPA PSAGAYSRAG VVKMTGGRA

LVS Predicted Coiled-Coil

QSIGRRGKVE QLSPEEEER RIRRE *RNKMA AAK

♠107x178x4♠

♥ALLMOTIS♥

♥CRNRREL ♠TDTLQAETDOLEDEKSALOTEIANLLKEKEKL♥

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

FIG. 44

7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDDEEAEEEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSVDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMLHLKKPGGFDISLFYRDIISIAEDED

♠107x178x4♠

♥ALLMOTIS♥

LVS Predicted Coiled-Coil

♥LRVH *FEE ♠SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE
ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK
IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS
DSFENPVLQQHFRNLEALALDLME

♣P12LZIPC♣

♣PEQAVDLTLPKVEAMNKRL♣ GSLVDEFKELVYPPDYNPEGKVTKR

KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG

LKKQELLEALTKHFQD

FIG. 45

7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♠107x178x4♠

♥ALLMOTIS♥

♥♠LTAWSRTLVTFKDVFVDEFTREEWKLLDT♠ AQQIVYRNV

MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEE VWKCR
DQLDKYQENPERHLRHQLIHTGEKPYECKEKGKSFSRSSHLIGHQKT
HTGEEPYECKEKGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKS FVH
SSRLIRHQRTHTGHKPYECPECKGKSFRQSTHLILHQRTHVVRPYECN
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSSRSHLYSHQRT
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♣P23LZIP♣

♣PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♣ RENAY

FIG. 46

7872-020 (SHEET 56 OF 63)

[illegible]

Fig. 49A

7872-020 (SHEET 57 OF 63)

HIV-1 BRU 178 Constructs, Mutations, Truncations									
Construct	178	179	180	181	182	183	184	185	186
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7872-020 (SHEET 60 OF 63)

EPSTEIN-BARR VIRUS STRAIN 895-8 BZLF1 TRANSGACTIVATOR PROTEIN EB1 OR ZEBRA		Residue		173		174		175		176		177		178		179		180		181		182		183		184		185		186		187		188		189		190		191		192		193		194		195		196		197		198		199		200		201		202		203		204		205		206		207		208		209		210		211		212		213		214		215		216		217		218		219		220		221		222		223		224		225		226		227		228		229		230		231		232		233		234		235		236		237		238		239		240		241		242		243		244		245		246		247		248		249		250		251		252		253		254		255		256		257		258		259		260		261		262		263		264		265		266		267		268		269		270		271		272		273		274		275		276		277		278		279		280		281		282		283		284		285		286		287		288		289		290		291		292		293		294		295		296		297		298		299		300		301		302		303		304		305		306		307		308		309		310		311		312		313		314		315		316		317		318		319		320		321		322		323		324		325		326		327		328		329		330		331		332		333		334		335		336		337		338		339		340		341		342		343		344		345		346		347		348		349		350		351		352		353		354		355		356		357		358		359		360		361		362		363		364		365		366		367		368		369		370		371		372		373		374		375		376		377		378		379		380		381		382		383		384		385		386		387		388		389		390		391		392		393		394		395		396		397		398		399		400		401		402		403		404		405		406		407		408		409		410		411		412		413		414		415		416		417		418		419		420		421		422		423		424		425		426		427		428		429		430		431		432		433		434		435		436		437		438		439		440		441		442		443		444		445		446		447		448		449		450		451		452		453		454		455		456		457		458		459		460		461		462		463		464		465		466		467		468		469		470		471		472		473		474		475		476		477		478		479		480		481		482		483		484		485		486		487		488		489		490		491		492		493		494		495		496		497		498		499		500		501		502		503		504		505		506		507		508		509		510		511		512		513		514		515		516		517		518		519		520		521		522		523		524		525		526		527		528		529		530		531		532		533		534		535		536		537		538		539		540		541		542		543		544		545		546		547		548		549		550		551		552		553		554		555		556		557		558		559		560		561		562		563		564		565		566		567		568		569		570		571		572		573		574		575		576		577		578		579		580		581		582		583		584		585		586		587		588		589		590		591		592		593		594		595		596		597		598		599		600		601		602		603		604		605		606		607		608		609		610		611		612		613		614		615		616		617		618		619		620		621		622		623		624		625		626		627		628		629		630		631		632		633		634		635		636		637		638		639	
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7872-020 (SHEET 61 OF 63)

Residue	197	L	Q	H	Y	R	E	V	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		46		
T-447	197	L	Q	H	Y	R	E	V	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I											232		35			
T-448	198	Q	H	Y	R	E	V	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R						233		35					
T-449	199	Q	H	Y	R	E	V	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R						234		35					
#	200		V	Y	R	E	V	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P					235		35				
T-451	201		R	E	V	A	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D					236		35				
T-452	202			E	V	A	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V				237		35				
T-453	203				V	A	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L			238		35				
T-454	204				A	A	A	A	A	K	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H		240		35				
T-455	205				A	A	A	A	A	K	S	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H		241		35			
T-456	206					A	A	A	A	K	S	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		35	
T-457	207					A	A	A	A	K	S	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		243		35	
T-458	208										S	S	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L		243		
Residue	209	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		246		37								
T-459	209	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L							244		35					
T-460	210	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		245		35								
T-461	211		N	D	R	L	R	L	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		246		35								

FIG. 51B

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Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

I=It. 52 A

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C07K 7/04, 14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/99

US CL : 530/324; 424/184.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1, 186.1, 187.1, 188.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, AIDSLINE, APS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 89, Number 21, issued November 1992, Wild et al, "A Synthetic Peptide Inhibitor of Human Immunodeficiency Virus Replication: Correlation Between Solution Structure and Viral Inhibition", pages 10537-41, see entire document.	1-3, 9, and 10 ----- 4-8 and 11-15

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	* T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
* A document defining the general state of the art which is not considered to be of particular relevance	* X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
* E earlier document published on or after the international filing date	* Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
* L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	* A document member of the same patent family
* O document referring to an oral disclosure, use, exhibition or other means	
* P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search 28 MARCH 1996	Date of mailing of the international search report 09 APR 1996
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 — 4-8 and 11-15
X — Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4 — 9 and 11
X — Y	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 5 — 9 and 12
X — Y	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	1 and 6 — 9 and 13
X — Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 — 9 and 14
P, Y	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15